GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 17.7662 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-9
Perfect score: 20
Sequence: 1 tagttaccctaattaaccta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17.4	87.0	511	9	US-10-301-480-56566	Sequence 56566, A
	2	17.4	87.0	511	10	US-10-301-480-669975	Sequence 669975,
	3	17.4	87.0	635	6	US-09-925-065A-563041	Sequence 563041,
	4	17.4	87.0	1323	6	US-09-925-065A-82927	Sequence 82927, A
	5	17.4	87.0	1323	9	US-10-301-480-29168	Sequence 29168, A
	6	17.4	87.0	1323	9	US-10-301-480-184167	Sequence 184167,
	7	17.4	87.0	1323	10	US-10-301-480-642577	Sequence 642577,
	8	17.4	87.0	1323	10	US-10-301-480-797576	Sequence 797576,
c	9	17.4	87.0	100137	9	US-10-330-773-620	Sequence 620, App
c	10	17.4	87.0	139573	10	US-10-506-513-3	Sequence 3, Appli
c	11	16.8	84.0	629	6	US-09-925-065A-340911	Sequence 340911,
c	12	16.8	84.0	629	6	US-09-925-065A-340912	Sequence 340912,
c	13	16.8	84.0	629	6	US-09-925-065A-340913	Sequence 340913,
c	14	16.8	84.0	642	6	US-09-925-065A-340914	Sequence 340914,
c	15	16.8	84.0	646	10	US-10-301-480-413849	Sequence 413849,
c'	16	16.8	84.0	646	10	US-10-301-480-413850	Sequence 413850,
c	17	16.8	84.0	646	10	US-10-301-480-413851	Sequence 413851,
c	18	16.8	84.0	646	10	US-10-301-480-1027258	Sequence 1027258,
c	19	16.8	84.0	646	10	US-10-301-480-1027259	Sequence 1027259,
c	20	16.8	84.0	646	10	US-10-301-480-1027260	Sequence 1027260,
c	21	16.8	84.0	3094	6	US-09-925-065A-717969	Sequence 717969,
c	22	16.8	84.0	3094	6	US-09-925-065A-717970	Sequence 717970,
c	23	16.8	84.0	3094	6	US-09-925-065A-717971	Sequence 717971,
c	24	16.8	84.0	3094	6	US-09-925-065A-717972	Sequence 717972,
c	25	16.8	84.0	3094	6	US-09-925-065A-717973	Sequence 717973,
c	26	16.8	84.0	3094	6	US-09-925-065A-717974	Sequence 717974,
c	27	16.8	84.0	3094	6	US-09-925-065A-717975	Sequence 717975,
c	28	16.8	84.0	3094	6	US-09-925-065A-717976	Sequence 717976,
c	29	16.8	84.0	3094	6	US-09-925-065A-717977	Sequence 717977,
c	30	16.4	82.0	700	6	US-09-925-065A-688196	Sequence 688196,
c	31	16	80.0	970	8	US-10-750-185-30148	Sequence 30148, A
c	32	16	80.0	970	8	US-10-750-623-30148	Sequence 30148, A
	33	15.8	79.0	462	6	US-09-925-065A-420236	Sequence 420236,
	34	15.8	79.0	473	10	US-10-301-480-485240	Sequence 485240,
	35	15.8	79.0	473	10	US-10-301-480-1098649	Sequence 1098649,
c	36	15.8	79.0	511	9	US-10-301-480-13900	Sequence 13900, A
c	37	15.8	79.0	511	10	US-10-301-480-627309	Sequence 627309,
c	38	15.8	79.0	513	10	US-10-301-480-243647	Sequence 243647,
c	39	15.8	79.0	513	10	US-10-301-480-243648	Sequence 243648,
c	40	15.8	79.0	513	10	US-10-301-480-857056	Sequence 857056,
c	41	15.8	79.0	513	10	US-10-301-480-857057	Sequence 857057,
c	42	15.8	79.0	517	6	US-09-925-065A-149561	Sequence 149561,
c	43	15.8	79.0	517	6	US-09-925-065A-149562	Sequence 149562,
	44	15.8	79.0	517	14	US-11-136-527-3431	Sequence 3431, Ap
	45	15.8	79.0	517	14	US-11-136-527-7527	Sequence 7527, Ap

ALIGNMENTS

RESULT 1
US-10-301-480-56566
; Sequence 56566, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56566
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-56566

Query Match 87.0%; Score 17.4; DB 9; Length 511;
Best Local Similarity 94.7%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TAGTTACCCTAATTAACCT 19
              ||||| ||||||||||||||
Db        432 TAGTTTCCCTAATTAACCT 450
```

RESULT 2
US-10-301-480-669975
; Sequence 669975, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 3.99328 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-9
Perfect score: 20
Sequence: 1 tagttaccctaattaaccta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16.4	82.0	67386	3	US-09-949-016-16519	Sequence 16519, A
c	2	15.8	79.0	601	3	US-09-949-016-133604	Sequence 133604,
c	3	15.8	79.0	212139	3	US-09-949-016-16065	Sequence 16065, A
c	4	15.8	79.0	245286	3	US-09-949-016-15497	Sequence 15497, A
	5	15.2	76.0	601	3	US-09-949-016-171671	Sequence 171671,
	6	15.2	76.0	601	3	US-09-949-002-4497	Sequence 4497, Ap
	7	15.2	76.0	1540	3	US-09-071-035-67	Sequence 67, Appl
	8	15.2	76.0	1540	3	US-10-206-576-67	Sequence 67, Appl
	9	15.2	76.0	1707	3	US-09-071-035-65	Sequence 65, Appl
	10	15.2	76.0	1707	3	US-10-206-576-65	Sequence 65, Appl
	11	15.2	76.0	1803	3	US-09-134-000C-2881	Sequence 2881, Ap
c	12	15.2	76.0	3722	3	US-10-164-595-9	Sequence 9, Appli
c	13	15.2	76.0	3862	3	US-10-164-595-5	Sequence 5, Appli
c	14	15.2	76.0	3937	3	US-10-164-595-7	Sequence 7, Appli
c	15	15.2	76.0	3985	3	US-10-164-595-3	Sequence 3, Appli
	16	15.2	76.0	36755	3	US-09-949-016-16994	Sequence 16994, A
	17	15.2	76.0	38059	3	US-09-328-925-4	Sequence 4, Appli
	18	15.2	76.0	91062	3	US-09-949-016-13019	Sequence 13019, A
	19	15.2	76.0	185765	3	US-09-949-002-674	Sequence 674, App
	20	15.2	76.0	185766	3	US-09-949-002-707	Sequence 707, App
c	21	15.2	76.0	298336	3	US-09-949-016-16600	Sequence 16600, A
c	22	15.2	76.0	421491	3	US-09-949-016-12805	Sequence 12805, A
c	23	15.2	76.0	421494	3	US-09-949-016-14060	Sequence 14060, A
	24	15.2	76.0	455726	3	US-09-949-016-14157	Sequence 14157, A
	25	15.2	76.0	481115	3	US-09-949-016-11940	Sequence 11940, A
	26	15.2	76.0	1230025	3	US-09-198-452A-1	Sequence 1, Appli
	27	15.2	76.0	1230230	3	US-09-438-185A-1	Sequence 1, Appli
c	28	15	75.0	601	3	US-09-949-016-80142	Sequence 80142, A
c	29	15	75.0	312470	3	US-09-949-016-14043	Sequence 14043, A
c	30	15	75.0	336024	3	US-09-949-016-12373	Sequence 12373, A
	31	14.8	74.0	228	3	US-09-489-039A-5795	Sequence 5795, Ap
c	32	14.8	74.0	252	3	US-09-489-039A-6239	Sequence 6239, Ap
	33	14.8	74.0	353	3	US-09-513-999C-1045	Sequence 1045, Ap
	34	14.8	74.0	468	3	US-09-513-999C-10440	Sequence 10440, A
c	35	14.8	74.0	601	3	US-09-949-016-26221	Sequence 26221, A
c	36	14.8	74.0	601	3	US-09-949-016-35377	Sequence 35377, A
c	37	14.8	74.0	601	3	US-09-949-016-41896	Sequence 41896, A
c	38	14.8	74.0	601	3	US-09-949-016-56207	Sequence 56207, A
c	39	14.8	74.0	601	3	US-09-949-016-74123	Sequence 74123, A
c	40	14.8	74.0	601	3	US-09-949-016-74154	Sequence 74154, A
c	41	14.8	74.0	601	3	US-09-949-016-123831	Sequence 123831,
c	42	14.8	74.0	601	3	US-09-949-016-205672	Sequence 205672,
c	43	14.8	74.0	807	3	US-09-270-767-29121	Sequence 29121, A
	44	14.8	74.0	815	3	US-09-328-111-23	Sequence 23, Appl
c	45	14.8	74.0	1322	3	US-09-270-767-4286	Sequence 4286, Ap

ALIGNMENTS

RESULT 1
US-09-949-016-16519
; Sequence 16519, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16519
; LENGTH: 67386
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(67386)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16519

Query Match 82.0%; Score 16.4; DB 3; Length 67386;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GTTACCCTAATTAACCTA 20
|||||| ||||||||||
Db 48082 GTTACCATAATTAACCTA 48099

RESULT 2
US-09-949-016-133604/c
; Sequence 133604, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 114.498 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-9
Perfect score: 20
Sequence: 1 tagttaccctaattaaccta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match	Length	DB	ID	Description
1		20	100.0	188	10	BX206435	BX206435 Danio rer
2		20	100.0	297	3	BM153964	BM153964 fv37b09.x
3		20	100.0	297	10	BX206839	BX206839 Danio rer
4		20	100.0	323	10	BX212086	BX212086 Danio rer
5		20	100.0	390	11	DR33K5T	AL985063 Danio rer
6		20	100.0	509	7	CK698900	CK698900 ZF101-P00
7	c	20	100.0	510	3	BI879062	BI879062 fm18e06.x
8	c	20	100.0	512	11	DR41D2S	AL983508 Danio rer
9		20	100.0	548	10	BX130901	BX130901 Danio rer
10	c	20	100.0	556	10	BX154360	BX154360 Danio rer
11		20	100.0	564	11	DR1I4S	AL733614 Danio rer
12	c	20	100.0	589	11	DR34F2S	AL975979 Danio rer
13		20	100.0	693	10	BX191816	BX191816 Danio rer
14	c	20	100.0	707	8	DN899849	DN899849 nap49h10.
15	c	20	100.0	727	10	BX192126	BX192126 Danio rer
16	c	20	100.0	728	10	BX221887	BX221887 Danio rer
17	c	20	100.0	770	7	CF998030	CF998030 AGENCOURT
18	c	20	100.0	771	10	BX205393	BX205393 Danio rer
19	c	20	100.0	772	10	BX177611	BX177611 Danio rer
20	c	20	100.0	776	7	CN511985	CN511985 AGENCOURT
21	c	20	100.0	781	10	BX220046	BX220046 Danio rer
22	c	20	100.0	785	10	BX137180	BX137180 Danio rer
23	c	20	100.0	797	10	BX234965	BX234965 Danio rer
24		20	100.0	802	10	BX129731	BX129731 Danio rer
25	c	20	100.0	805	7	CN505208	CN505208 AGENCOURT
26		20	100.0	812	10	BX223505	BX223505 Danio rer
27	c	20	100.0	821	10	BX206804	BX206804 Danio rer
28	c	20	100.0	824	10	BX156069	BX156069 Danio rer
29	c	20	100.0	831	7	CN170393	CN170393 AGENCOURT
30	c	20	100.0	861	6	CD760369	CD760369 AGENCOURT
31		20	100.0	896	6	CF594812	CF594812 AGENCOURT
32	c	20	100.0	919	6	CA474743	CA474743 AGENCOURT
33	c	20	100.0	934	6	CA474833	CA474833 AGENCOURT
34	c	19	95.0	350	10	BX158466	BX158466 Danio rer
35	c	19	95.0	490	10	BX247732	BX247732 Danio rer
36	c	19	95.0	492	3	BM024443	BM024443 fu47d09.y
37	c	19	95.0	645	11	DR48H10T	AL980644 Danio rer
38		19	95.0	708	8	DN857131	DN857131 naa10c04.
39		19	95.0	758	6	CB571304	CB571304 AGENCOURT
40		19	95.0	813	10	BX210720	BX210720 Danio rer
41		19	95.0	857	10	BX181115	BX181115 Danio rer
42		18.4	92.0	228	3	BI845756	BI845756 fs96h05.x
43	c	18.4	92.0	244	10	BX131174	BX131174 Danio rer
44	c	18.4	92.0	269	10	BX232465	BX232465 Danio rer
45	c	18.4	92.0	271	10	BX244148	BX244148 Danio rer

ALIGNMENTS

RESULT 1
BX206435
LOCUS BX206435 188 bp DNA linear GSS 29-JAN-2003
DEFINITION Danio rerio genomic clone DKEY-238J19, genomic survey sequence.
ACCESSION BX206435
VERSION BX206435.1 GI:28038321
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 188)
AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 238J19. 238J19 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES Location/Qualifiers
source 1. .188
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-238J19"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 188;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAGTTACCCTAATTAACCTA 20
||||||||||||||||||||
Db 55 TAGTTACCCTAATTAACCTA 74

RESULT 2
BM153964
LOCUS BM153964 297 bp mRNA linear EST 30-NOV-2001
DEFINITION fv37b09.x1 Sugano SJD adult male Danio rerio cDNA clone

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 16.3691 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-9
Perfect score: 20
Sequence: 1 tagttaccctaattaaccta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	100.0	20	13	ADT08250	Adt08250 Zebrafish
2	20	100.0	20	13	ADT89058	Adt89058 Zebrafish
3	20	100.0	435	13	ADT08242	Adt08242 Zebrafish
4	20	100.0	435	13	ADT89050	Adt89050 Zebrafish
5	20	100.0	480	13	ADT08271	Adt08271 Zebrafish
6	20	100.0	480	13	ADT89079	Adt89079 Zebrafish
7	20	100.0	2033	13	ADT08244	Adt08244 Zebrafish
8	20	100.0	2033	13	ADT89052	Adt89052 Zebrafish
9	20	100.0	2783	13	ADT08243	Adt08243 Zebrafish
10	20	100.0	2783	13	ADT89051	Adt89051 Zebrafish
11	20	100.0	2960	13	ADT89080	Adt89080 Zebrafish
c 12	18.4	92.0	3003	10	ADF18692	Adf18692 Zebrafish
13	18.4	92.0	13382	14	ADW44488	Adw44488 Zebrafish
c 14	18.4	92.0	13382	14	ADW44488	Adw44488 Zebrafish
c 15	17.4	87.0	100137	12	ADQ97643	Adq97643 Human can
c 16	17.4	87.0	139573	10	ADH58564	Adh58564 Human Na+
c 17	17.4	87.0	156416	13	ABD32817	Abd32817 Human can
c 18	16.8	84.0	5563	2	AAX08941	Aax08941 GATA-1 pr
c 19	16.8	84.0	8346	6	ABK28328	Abk28328 DNA trans
20	16.8	84.0	78064	13	ADS17402	Ads17402 Nucleotid
c 21	16.8	84.0	96599	10	ADC85298	Adc85298 Human Egr
c 22	16.8	84.0	96600	9	ADA02819	Ada02819 Mouse Sos
c 23	16.8	84.0	96600	10	ADB72557	Adb72557 Mouse Sos
c 24	16.8	84.0	96600	12	ADM74414	Adm74414 Murine ca
c 25	16.4	82.0	110000	12	ADN46845_04	Continuation (5 of
26	16.4	82.0	110000	12	ADN47591_16	Continuation (17 o
c 27	16.4	82.0	110000	12	ADN46123_04	Continuation (5 of
28	16.4	82.0	110000	12	ADN47209_16	Continuation (17 o
c 29	16.4	82.0	110000	12	ADN46464_04	Continuation (5 of
30	16.4	82.0	110000	12	ADN47960_16	Continuation (17 o
31	16	80.0	2000	11	ACL34957	Acl34957 Rice stre
c 32	15.8	79.0	389	10	ACD93134	Acd93134 Human col
c 33	15.8	79.0	401	4	AAK95767	Aak95767 Human neu
c 34	15.8	79.0	401	4	AAK95768	Aak95768 Human neu
c 35	15.8	79.0	401	4	AAK95766	Aak95766 Human neu
c 36	15.8	79.0	401	4	AAK97261	Aak97261 Human neu
c 37	15.8	79.0	401	4	AAK97260	Aak97260 Human neu
c 38	15.8	79.0	401	4	AAK97259	Aak97259 Human neu
c 39	15.8	79.0	401	6	ABT00537	Abt00537 Human neu
c 40	15.8	79.0	401	6	ABT00538	Abt00538 Human neu
c 41	15.8	79.0	401	6	ABT00536	Abt00536 Human neu
c 42	15.8	79.0	401	6	ABT02030	Abt02030 Human neu
c 43	15.8	79.0	401	6	ABT02029	Abt02029 Human neu
c 44	15.8	79.0	401	6	ABT02031	Abt02031 Human neu
45	15.8	79.0	426	6	ABN66455	Abn66455 Streptoco

ALIGNMENTS

RESULT 1
ADT08250
ID ADT08250 standard; DNA; 20 BP.
XX
AC ADT08250;
XX
DT 13-JAN-2005 (first entry)
XX
DE Zebrafish L-FABP upstream region PDX2 binding site.
XX
KW Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer.
XX
OS Danio rerio.
XX
PN US2004209833-A1.
XX
PD 21-OCT-2004.
XX
PF 21-NOV-2003; 2003US-00717573.
XX
PR 16-APR-2003; 2003US-0463035P.
PR 27-MAY-2003; 2003US-0473210P.
XX
PA (WUJJ/) WU J.
PA (HERG/) HER G M.
XX
PI Wu J, Her GM;
XX
DR WPI; 2004-765481/75.
XX
PT New isolated polynucleotide useful for generating transgenic fish such as
PT zebrafish, comprises liver-specific expression control sequence that
PT modulates expression of vertebrate liver fatty acid binding protein.
XX
PS Claim 5; SEQ ID NO 9; 40pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a liver-
CC specific expression control sequence (LR) which modulates expression of a
CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 118.984 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-9
Perfect score: 20
Sequence: 1 tagttaccctaattaaccta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		20	100.0	2960	5	AF512998	AF512998 Danio rer
2	c	20	100.0	13481	5	DRE251640	AJ251640 Danio rer
3	c	20	100.0	16353	5	CR352254	CR352254 Zebrafish
4	c	20	100.0	36855	5	BX544873	BX544873 Zebrafish
5	c	20	100.0	39600	14	CR361567	CR361567 Danio rer
6	c	20	100.0	43083	5	CR848679	CR848679 Zebrafish
7	c	20	100.0	46016	5	CR381556	CR381556 Zebrafish
8		20	100.0	51065	5	CR936321	CR936321 Zebrafish
9		20	100.0	52968	5	BX927067	BX927067 Zebrafish
10		20	100.0	55248	5	CR855395	CR855395 Zebrafish
11		20	100.0	55372	14	CR759965	CR759965 Danio rer
12		20	100.0	57807	5	CR848002	CR848002 Zebrafish
13		20	100.0	58279	5	CR854925	CR854925 Zebrafish
14	c	20	100.0	58949	14	BX649482_3	Continuation (4 of
15		20	100.0	61341	5	BX666063	BX666063 Zebrafish
16		20	100.0	64210	5	CR388084	CR388084 Zebrafish
17	c	20	100.0	71474	5	CR855380	CR855380 Zebrafish
18		20	100.0	73207	5	BX914202	BX914202 Zebrafish
19	c	20	100.0	73894	5	BX296559	BX296559 Zebrafish
20		20	100.0	74464	5	BX294187	BX294187 Zebrafish
21		20	100.0	76812	5	BX855614	BX855614 Zebrafish
22		20	100.0	80226	5	BX323582	BX323582 Zebrafish
23	c	20	100.0	82797	14	BX890561_3	Continuation (4 of
24		20	100.0	86183	5	BX469918	BX469918 Zebrafish
25	c	20	100.0	87559	5	BX571814	BX571814 Zebrafish
26		20	100.0	88824	5	CR933839	CR933839 Zebrafish
27		20	100.0	89050	5	CR536610	CR536610 Zebrafish
28	c	20	100.0	90347	5	AL714030	AL714030 Zebrafish
29	c	20	100.0	91311	5	CR356238	CR356238 Zebrafish
30		20	100.0	91343	14	CT009673	CT009673 Danio rer
31	c	20	100.0	91343	14	CT009673	CT009673 Danio rer
32	c	20	100.0	91362	5	BX950869	BX950869 Zebrafish
33		20	100.0	92348	5	AL935295	AL935295 Zebrafish
34	c	20	100.0	92637	5	BX855615	BX855615 Zebrafish
35	c	20	100.0	93244	14	CT009621	CT009621 Danio rer
36	c	20	100.0	93602	14	CT009592	CT009592 Danio rer
37	c	20	100.0	94103	5	AL845545	AL845545 Zebrafish
38		20	100.0	95153	14	CR954248	CR954248 Danio rer
39	c	20	100.0	95674	5	CR759816	CR759816 Zebrafish
40	c	20	100.0	95798	5	AL954721	AL954721 Zebrafish
41		20	100.0	98080	14	CR925801	CR925801 Danio rer
42	c	20	100.0	98080	14	CR925801	CR925801 Danio rer
43		20	100.0	98407	14	CR383670	CR383670 Danio rer
44		20	100.0	99186	14	AL732580	AL732580 Danio rer
45	c	20	100.0	99186	14	AL732580	AL732580 Danio rer

ALIGNMENTS

RESULT 1
AF512998
LOCUS AF512998 2960 bp DNA linear VRT 10-JUL-2003
DEFINITION Danio rerio liver-type fatty acid binding protein gene, partial cds.
ACCESSION AF512998
VERSION AF512998.1 GI:21314558
KEYWORDS .
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 2960)
AUTHORS Her,G.M., Yeh,Y.H. and Wu,J.L.
TITLE 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish
JOURNAL Dev. Dyn. 227 (3), 347-356 (2003)
PUBMED 12815620
REFERENCE 2 (bases 1 to 2960)
AUTHORS Her,G.M. and Wu,J.-L.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chiu-Yuan Road, Sec. 2, Taipei 115, Taiwan
FEATURES Location/Qualifiers
source 1. .2960
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
mRNA <2784. .>2960
/product="liver-type fatty acid binding protein"
CDS 2784. .>2960
/note="Lfabp; small cytosolic protein involved in lipid transport and metabolism"
/codon_start=1
/product="liver-type fatty acid binding protein"
/protein_id="AAM47005.1"
/db_xref="GI:21314559"
/translation="MAFSGTWQVYAQENYEEFLRAISLPEEVIKLAKDVKPVTEIQQN GSDFTITSKTPGKTV"

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 23.3171 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-9
Perfect score: 20
Sequence: 1 tagttaccctaattaaccta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	8	US-10-677-254-9	Sequence 9, Appli
	2	20	100.0	20	8	US-10-717-573-9	Sequence 9, Appli
	3	20	100.0	435	8	US-10-677-254-1	Sequence 1, Appli
	4	20	100.0	435	8	US-10-717-573-1	Sequence 1, Appli
	5	20	100.0	480	8	US-10-677-254-30	Sequence 30, Appl
	6	20	100.0	480	8	US-10-717-573-30	Sequence 30, Appl
	7	20	100.0	2033	8	US-10-677-254-3	Sequence 3, Appli
	8	20	100.0	2033	8	US-10-717-573-3	Sequence 3, Appli
	9	20	100.0	2783	8	US-10-677-254-2	Sequence 2, Appli
	10	20	100.0	2783	8	US-10-717-573-2	Sequence 2, Appli
c	11	18.4	92.0	3003	9	US-10-511-362-9	Sequence 9, Appli
	12	18.4	92.0	13382	8	US-10-612-594-4	Sequence 4, Appli
c	13	18.4	92.0	13382	8	US-10-612-594-4	Sequence 4, Appli
	14	17.4	87.0	527	5	US-10-027-632-204324	Sequence 204324,
	15	17.4	87.0	527	6	US-10-027-632-204324	Sequence 204324,
	16	17.4	87.0	635	4	US-09-925-065A-563041	Sequence 563041,
	17	17.4	87.0	1323	4	US-09-925-065A-82927	Sequence 82927, A
c	18	17.4	87.0	156416	9	US-10-461-862-12	Sequence 12, Appl
c	19	16.8	84.0	570	7	US-10-242-535A-51290	Sequence 51290, A
c	20	16.8	84.0	570	7	US-10-085-783A-51290	Sequence 51290, A
c	21	16.8	84.0	629	4	US-09-925-065A-340911	Sequence 340911,
c	22	16.8	84.0	629	4	US-09-925-065A-340912	Sequence 340912,
c	23	16.8	84.0	629	4	US-09-925-065A-340913	Sequence 340913,
c	24	16.8	84.0	642	4	US-09-925-065A-340914	Sequence 340914,
c	25	16.8	84.0	3094	4	US-09-925-065A-717969	Sequence 717969,
c	26	16.8	84.0	3094	4	US-09-925-065A-717970	Sequence 717970,
c	27	16.8	84.0	3094	4	US-09-925-065A-717971	Sequence 717971,
c	28	16.8	84.0	3094	4	US-09-925-065A-717972	Sequence 717972,
c	29	16.8	84.0	3094	4	US-09-925-065A-717973	Sequence 717973,
c	30	16.8	84.0	3094	4	US-09-925-065A-717974	Sequence 717974,
c	31	16.8	84.0	3094	4	US-09-925-065A-717975	Sequence 717975,
c	32	16.8	84.0	3094	4	US-09-925-065A-717976	Sequence 717976,
c	33	16.8	84.0	3094	4	US-09-925-065A-717977	Sequence 717977,
c	34	16.8	84.0	5563	5	US-10-136-734-26	Sequence 26, Appl
c	35	16.8	84.0	8346	6	US-10-240-453-202	Sequence 202, App
c	36	16.8	84.0	96600	3	US-09-997-722-85	Sequence 85, Appl
c	37	16.4	82.0	700	4	US-09-925-065A-688196	Sequence 688196,
c	38	15.8	79.0	401	3	US-09-795-668-565	Sequence 565, App
c	39	15.8	79.0	401	3	US-09-795-668-566	Sequence 566, App
c	40	15.8	79.0	401	3	US-09-795-668-567	Sequence 567, App
c	41	15.8	79.0	401	3	US-09-795-686-565	Sequence 565, App
c	42	15.8	79.0	401	3	US-09-795-686-566	Sequence 566, App
c	43	15.8	79.0	401	3	US-09-795-686-567	Sequence 567, App
c	44	15.8	79.0	401	3	US-09-946-807-565	Sequence 565, App
c	45	15.8	79.0	401	3	US-09-946-807-566	Sequence 566, App

ALIGNMENTS

RESULT 1
US-10-677-254-9
; Sequence 9, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-9

Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TAGTTACCCTAATTAACCTA 20
              ||||||||||||||||||||
Db          1 TAGTTACCCTAATTAACCTA 20
```

RESULT 2
US-10-717-573-9
; Sequence 9, Application US/10717573
; Publication No. US20040209833A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/717,573
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 4.19294 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-8
Perfect score: 21
Sequence: 1 tgacttgcctaattaccctaa 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	17	81.0	601	3	US-09-949-002-8712	Sequence 8712, Ap
c	2	16.8	80.0	601	3	US-09-949-016-34841	Sequence 34841, A
c	3	16.8	80.0	601	3	US-09-949-016-34842	Sequence 34842, A
c	4	16.8	80.0	601	3	US-09-949-016-73452	Sequence 73452, A
c	5	16.8	80.0	601	3	US-09-949-016-73453	Sequence 73453, A
c	6	16.8	80.0	601	3	US-09-949-016-153876	Sequence 153876,
c	7	16.8	80.0	174029	3	US-09-949-016-12610	Sequence 12610, A
c	8	16.8	80.0	174030	3	US-09-949-016-13880	Sequence 13880, A
c	9	16.8	80.0	248968	3	US-09-949-016-12614	Sequence 12614, A
c	10	16.8	80.0	250958	3	US-09-949-016-16061	Sequence 16061, A
	11	16.4	78.1	5000	3	US-09-791-105B-2	Sequence 2, Appli
	12	16.4	78.1	102053	3	US-09-949-016-13025	Sequence 13025, A
	13	16.4	78.1	118999	3	US-09-791-105B-32	Sequence 32, Appl
c	14	16.4	78.1	300598	3	US-09-949-016-11868	Sequence 11868, A
c	15	16.4	78.1	302604	3	US-09-949-016-14588	Sequence 14588, A
c	16	16.4	78.1	302604	3	US-09-949-016-14589	Sequence 14589, A
c	17	16.4	78.1	308362	3	US-09-949-016-17119	Sequence 17119, A
	18	16.2	77.1	601	3	US-09-949-016-141554	Sequence 141554,
	19	16.2	77.1	984	3	US-09-792-024-21	Sequence 21, Appl
	20	16.2	77.1	1060	3	US-09-949-016-3687	Sequence 3687, Ap
	21	16.2	77.1	2695	3	US-10-104-047-1364	Sequence 1364, Ap
c	22	16.2	77.1	4598	3	US-09-949-016-16434	Sequence 16434, A
c	23	16.2	77.1	39176	3	US-09-949-016-17603	Sequence 17603, A
	24	16.2	77.1	110266	3	US-09-949-016-14913	Sequence 14913, A
	25	16.2	77.1	110266	3	US-09-949-016-14914	Sequence 14914, A
	26	16.2	77.1	110266	3	US-09-949-016-14915	Sequence 14915, A
	27	16.2	77.1	110266	3	US-09-949-016-14916	Sequence 14916, A
	28	16.2	77.1	110266	3	US-09-949-016-14917	Sequence 14917, A
	29	16.2	77.1	110266	3	US-09-949-016-14918	Sequence 14918, A
	30	16.2	77.1	110266	3	US-09-949-016-14919	Sequence 14919, A
	31	16.2	77.1	110266	3	US-09-949-016-14920	Sequence 14920, A
	32	16.2	77.1	110266	3	US-09-949-016-14921	Sequence 14921, A
	33	16.2	77.1	110266	3	US-09-949-016-14922	Sequence 14922, A
	34	16.2	77.1	132762	3	US-09-954-556-17	Sequence 17, Appl
	35	16.2	77.1	236341	3	US-09-949-016-13978	Sequence 13978, A
c	36	16.2	77.1	236964	3	US-09-949-016-15753	Sequence 15753, A
	37	16	76.2	209631	3	US-09-949-002-574	Sequence 574, App
	38	16	76.2	209632	3	US-09-949-002-802	Sequence 802, App
	39	15.8	75.2	700	3	US-09-735-271-961	Sequence 961, App
	40	15.8	75.2	38261	3	US-09-949-016-13802	Sequence 13802, A
	41	15.8	75.2	221545	3	US-09-949-016-13875	Sequence 13875, A
	42	15.4	73.3	601	3	US-09-949-016-135767	Sequence 135767,
c	43	15.4	73.3	601	3	US-09-949-016-162532	Sequence 162532,
c	44	15.4	73.3	7127	3	US-09-435-376-3	Sequence 3, Appli
	45	15.4	73.3	24214	3	US-09-949-016-15551	Sequence 15551, A

ALIGNMENTS

RESULT 1
US-09-949-002-8712/c
; Sequence 8712, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8712
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-8712

Query Match 81.0%; Score 17; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 23;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TGACTTGCCTAATTACCCT 19
              |: |||||||||||||||||
Db        302 TKTCTTGCCTAATTACCCT 284
```

RESULT 2
US-09-949-016-34841/c
; Sequence 34841, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 120.222 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-8
Perfect score: 21
Sequence: 1 tgacttgcctaattaccctaa 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	169	10	BX124567	BX124567 Danio rer
c 2	21	100.0	253	3	BM025481	BM025481 fs79b01.y
c 3	21	100.0	261	7	CN841194	CN841194 AGENCOURT
4	21	100.0	297	6	CD606335	CD606335 RZ151A1F1
5	21	100.0	318	10	BX237207	BX237207 Danio rer
c 6	21	100.0	340	6	CD597232	CD597232 RK103A2E0
c 7	21	100.0	340	6	CD601394	CD601394 RK132A2F0
c 8	21	100.0	349	6	CD601336	CD601336 RK132A1E0
c 9	21	100.0	350	6	CD592661	CD592661 RK073A2E0
10	21	100.0	364	6	CD585167	CD585167 RK029A4E0
11	21	100.0	379	10	BX163569	BX163569 Danio rer
12	21	100.0	404	1	AL731242	AL731242 AL731242
13	21	100.0	412	11	DR38A22S	AL974517 Danio rer
14	21	100.0	415	3	BM026582	BM026582 ft07h09.x
15	21	100.0	421	3	BI983218	BI983218 fu45g04.x
c 16	21	100.0	427	3	BM026426	BM026426 ft07h09.y
c 17	21	100.0	431	1	AI878137	AI878137 fc57h07.y
c 18	21	100.0	431	2	BG985624	BG985624 5069 NICH
19	21	100.0	435	1	AI878419	AI878419 fc57h07.x
c 20	21	100.0	442	1	AI943080	AI943080 fc84a05.x
c 21	21	100.0	444	3	BM155502	BM155502 fw06f01.y
22	21	100.0	446	1	AL910060	AL910060 AL910060
23	21	100.0	453	3	BI430094	BI430094 fs87h10.x
24	21	100.0	456	3	BI476314	BI476314 fq26e07.x
c 25	21	100.0	462	1	AI667066	AI667066 fc37c02.x
c 26	21	100.0	463	1	AI396940	AI396940 fb07e03.x
c 27	21	100.0	464	2	BE201284	BE201284 fk89c10.y
28	21	100.0	466	3	BI428752	BI428752 fr73a01.x
c 29	21	100.0	468	6	CB352105	CB352105 ZF001-P00
30	21	100.0	477	1	AI545438	AI545438 fb81c03.x
31	21	100.0	483	3	BM071181	BM071181 fv03h04.x
32	21	100.0	489	10	BX167558	BX167558 Danio rer
33	21	100.0	492	1	AI878707	AI878707 fc64g04.x
34	21	100.0	498	1	AW826633	AW826633 fk55a12.x
35	21	100.0	504	11	DR35J16S	AL979317 Danio rer
36	21	100.0	505	3	BI840860	BI840860 fq39f10.x
c 37	21	100.0	514	11	DR46O9T	AL982918 Danio rer
c 38	21	100.0	518	3	BI880089	BI880089 fm69f06.x
39	21	100.0	520	1	AL928427	AL928427 AL928427
c 40	21	100.0	523	3	BM531885	BM531885 fx92c11.y
c 41	21	100.0	523	6	CB359375	CB359375 ZF001-P00
c 42	21	100.0	530	3	BI430060	BI430060 fs87h10.y
43	21	100.0	536	3	BI428231	BI428231 fr76c09.x
44	21	100.0	539	7	CR928386	CR928386 CR928386
45	21	100.0	542	3	BI325511	BI325511 fr39b08.x

ALIGNMENTS

RESULT 1
BX124567
LOCUS BX124567 169 bp DNA linear GSS 13-MAR-2003
DEFINITION Danio rerio genomic clone DKEY-65A3, genomic survey sequence.
ACCESSION BX124567
VERSION BX124567.1 GI:27955505
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 169)
AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the SP6 end of BAC 65A3. 65A3 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES Location/Qualifiers
source 1. .169
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-65A3"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
ORIGIN

Query Match 100.0%; Score 21; DB 10; Length 169;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTTGCCTAATTACCCTAA 21
||||||||||||||||||||
Db 76 TGACTTGCCTAATTACCCTAA 96

RESULT 2
BM025481/c
LOCUS BM025481 253 bp mRNA linear EST 30-OCT-2001
DEFINITION fs79b01.y1 Zebrafish SJD day 8 fin regeneration Danio rerio cDNA

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 17.1875 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-8
Perfect score: 21
Sequence: 1 tgacttgcctaattaccctaa 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	13	ADT08249	Adt08249 Zebrafish
	2	21	100.0	21	13	ADT89057	Adt89057 Zebrafish
	3	21	100.0	435	13	ADT08242	Adt08242 Zebrafish
	4	21	100.0	435	13	ADT89050	Adt89050 Zebrafish
	5	21	100.0	480	13	ADT08271	Adt08271 Zebrafish
	6	21	100.0	480	13	ADT89079	Adt89079 Zebrafish
	7	21	100.0	2033	13	ADT08244	Adt08244 Zebrafish
	8	21	100.0	2033	13	ADT89052	Adt89052 Zebrafish
	9	21	100.0	2783	13	ADT08243	Adt08243 Zebrafish
	10	21	100.0	2783	13	ADT89051	Adt89051 Zebrafish
	11	21	100.0	2960	13	ADT89080	Adt89080 Zebrafish
c	12	19.4	92.4	7495	13	ADR30815	Adr30815 Zebrafish
c	13	19.4	92.4	7508	13	ADR30814	Adr30814 Zebrafish
c	14	19.4	92.4	71843	8	ACC79619	Acc79619 Zebrafish
	15	17.8	84.8	13382	14	ADW44488	Adw44488 Zebrafish
c	16	17.8	84.8	78064	13	ADS17402	Ads17402 Nucleotid
	17	16.8	80.0	78064	13	ADS17402	Ads17402 Nucleotid
	18	16.4	78.1	5000	4	AAS14506	Aas14506 Human GST
c	19	16.4	78.1	6070	6	ABL33679	Abl33679 Human imm
c	20	16.4	78.1	6070	6	ABL34579	Abl34579 Human met
c	21	16.4	78.1	6070	6	ABL70372	Abl70372 Chemicall
c	22	16.4	78.1	6070	6	ABQ67130	Abq67130 Human ang
c	23	16.4	78.1	6070	7	ADS99840	Ads99840 Complemen
c	24	16.4	78.1	6197	6	ABN80256	Abn80256 Human che
c	25	16.4	78.1	7049	6	ABL32156	Abl32156 Human imm
c	26	16.4	78.1	7049	6	ABL54305	Abl54305 Chemicall
c	27	16.4	78.1	10716	6	ABL33418	Abl33418 Human imm
c	28	16.4	78.1	33053	6	ABQ67006	Abq67006 Human ang
c	29	16.4	78.1	34548	6	ABL70604	Abl70604 Chemicall
c	30	16.4	78.1	37973	6	ABL34196	Abl34196 Human imm
c	31	16.4	78.1	73334	6	ABL34125	Abl34125 Human imm
c	32	16.4	78.1	73334	6	ABL92319	Abl92319 Chemicall
c	33	16.4	78.1	76798	6	ABN97454	Abn97454 Gene #395
c	34	16.4	78.1	76798	14	ADX06902	Adx06902 Cyclin-de
c	35	16.4	78.1	83391	6	ABQ67093	Abq67093 Human ang
	36	16.2	77.1	401	9	ACH48896	Ach48896 Human leu
	37	16.2	77.1	431	5	AAS83152	Aas83152 DNA encod
	38	16.2	77.1	431	12	ADO40991	Ado40991 Human cDN
	39	16.2	77.1	441	4	ABA89222	Aba89222 Escherich
	40	16.2	77.1	501	12	ACH74075	Ach74075 Human gen
c	41	16.2	77.1	512	12	ACH71469	Ach71469 Human gen
	42	16.2	77.1	559	9	ACH16166	Ach16166 Human adu
c	43	16.2	77.1	587	4	AAS25471	Aas25471 Human ova
	44	16.2	77.1	621	3	AAA05868	Aaa05868 Group B S
	45	16.2	77.1	636	13	ACN51439	Acn51439 Cotton an

ALIGNMENTS

RESULT 1
ADT08249
ID ADT08249 standard; DNA; 21 BP.
XX
AC ADT08249;
XX
DT 13-JAN-2005 (first entry)
XX
DE Zebrafish L-FABP upstream region PDX1 binding site.
XX
KW Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer.
XX
OS Danio rerio.
XX
PN US2004209833-A1.
XX
PD 21-OCT-2004.
XX
PF 21-NOV-2003; 2003US-00717573.
XX
PR 16-APR-2003; 2003US-0463035P.
PR 27-MAY-2003; 2003US-0473210P.
XX
PA (WUJJ/) WU J.
PA (HERG/) HER G M.
XX
PI Wu J, Her GM;
XX
DR WPI; 2004-765481/75.
XX
PT New isolated polynucleotide useful for generating transgenic fish such as
PT zebrafish, comprises liver-specific expression control sequence that
PT modulates expression of vertebrate liver fatty acid binding protein.
XX
PS Claim 5; SEQ ID NO 8; 40pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a liver-
CC specific expression control sequence (LR) which modulates expression of a
CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 124.933 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-8
Perfect score: 21
Sequence: 1 tgacttgcctaattaccctaa 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		21	100.0	1579	5	BC095039	BC095039 Danio rer
c 2		21	100.0	1650	5	DRTKRAL1	Y09669 D.rerio mRN
3		21	100.0	2065	5	BC076409	BC076409 Danio rer
c 4		21	100.0	2191	5	BC044395	BC044395 Danio rer
c 5		21	100.0	2635	5	BC076547	BC076547 Danio rer
6		21	100.0	2905	5	BC092170	BC092170 Danio rer
7		21	100.0	2960	5	AF512998	AF512998 Danio rer
c 8		21	100.0	16353	5	CR352254	CR352254 Zebrafish
c 9		21	100.0	23743	5	CR376835	CR376835 Zebrafish
c 10		21	100.0	29988	14	CR762446_5	Continuation (6 of
11		21	100.0	31940	5	CR385072	CR385072 Zebrafish
12		21	100.0	32786	5	BX571835	BX571835 Zebrafish
c 13		21	100.0	38062	14	CR759876	CR759876 Danio rer
14		21	100.0	39233	5	CR388362	CR388362 Zebrafish
c 15		21	100.0	39767	5	BX255959	BX255959 Zebrafish
c 16		21	100.0	41950	5	BX649278	BX649278 Zebrafish
c 17		21	100.0	42660	5	CR556724	CR556724 Zebrafish
18		21	100.0	43563	5	BX470103	BX470103 Zebrafish
19		21	100.0	44797	5	CR753881	CR753881 Zebrafish
c 20		21	100.0	47275	5	BX897669	BX897669 Zebrafish
c 21		21	100.0	47333	5	AL928934	AL928934 Zebrafish
c 22		21	100.0	47442	14	AC146465	AC146465 Danio rer
c 23		21	100.0	49875	5	BX510921	BX510921 Zebrafish
24		21	100.0	50111	5	CR762393	CR762393 Zebrafish
25		21	100.0	50895	5	AL732386	AL732386 Zebrafish
c 26		21	100.0	51808	5	AC104683	AC104683 Danio rer
27		21	100.0	52909	14	CR753895_3	Continuation (4 of
28		21	100.0	53370	5	AC144825	AC144825 Danio rer
c 29		21	100.0	53530	5	CR388040	CR388040 Zebrafish
30		21	100.0	54100	14	CR848730	CR848730 Danio rer
c 31		21	100.0	57059	5	CR450822	CR450822 Zebrafish
c 32		21	100.0	58039	5	CR759821	CR759821 Zebrafish
33		21	100.0	58124	5	CR937028	CR937028 Zebrafish
34		21	100.0	58638	5	BX248388	BX248388 Zebrafish
c 35		21	100.0	60081	14	BX088711_3	Continuation (4 of
c 36		21	100.0	61341	5	BX666063	BX666063 Zebrafish
c 37		21	100.0	62252	5	BX322549	BX322549 Zebrafish
c 38		21	100.0	62994	5	BX255886	BX255886 Zebrafish
39		21	100.0	63779	5	AL845322	AL845322 Zebrafish
c 40		21	100.0	64422	5	BX897748	BX897748 Zebrafish
41		21	100.0	67061	14	CR354609_3	Continuation (4 of
c 42		21	100.0	67355	14	BX649395_3	Continuation (4 of
c 43		21	100.0	67817	5	BX950227	BX950227 Zebrafish
c 44		21	100.0	69669	5	AL591664	AL591664 Zebrafish
c 45		21	100.0	70420	5	BX470074	BX470074 Zebrafish

ALIGNMENTS

RESULT 1
BC095039
LOCUS BC095039 1579 bp mRNA linear VRT 06-JUN-2005
DEFINITION Danio rerio zgc:109899, mRNA (cDNA clone MGC:109899 IMAGE:7225575), complete cds.
ACCESSION BC095039
VERSION BC095039.1 GI:63101752
KEYWORDS MGC.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 1579)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
CONSRTM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 1579)
AUTHORS .
CONSRTM NIH MGC Project
TITLE Direct Submission

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 18.6545 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-8
Perfect score: 21
Sequence: 1 tgacttgcctaattaccctaa 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	17.8	84.8	3417	8	US-10-750-185-33312	Sequence 33312, A
	2	17.8	84.8	3417	8	US-10-750-623-33312	Sequence 33312, A
	3	17.8	84.8	188682	14	US-11-112-908-23	Sequence 23, Appl
	4	17.4	82.9	1076	6	US-09-925-065A-699655	Sequence 699655,
	5	17.4	82.9	1076	6	US-09-925-065A-699656	Sequence 699656,
	6	17	81.0	555	10	US-10-301-480-418788	Sequence 418788,
	7	17	81.0	555	10	US-10-301-480-1032197	Sequence 1032197,
c	8	17	81.0	561	6	US-09-925-065A-346440	Sequence 346440,
	9	17	81.0	600	6	US-09-925-065A-729651	Sequence 729651,
c	10	17	81.0	606	6	US-09-925-065A-776627	Sequence 776627,
c	11	17	81.0	606	6	US-09-925-065A-776628	Sequence 776628,
	12	17	81.0	609	6	US-09-925-065A-763839	Sequence 763839,
	13	17	81.0	1225	8	US-10-750-185-61932	Sequence 61932, A
	14	17	81.0	1225	8	US-10-750-623-61932	Sequence 61932, A
	15	16.8	80.0	420	6	US-09-925-065A-656611	Sequence 656611,
	16	16.8	80.0	583	6	US-09-925-065A-375086	Sequence 375086,
	17	16.8	80.0	587	10	US-10-301-480-444828	Sequence 444828,
	18	16.8	80.0	587	10	US-10-301-480-1058237	Sequence 1058237,
	19	16.4	78.1	554	6	US-09-925-065A-652951	Sequence 652951,
	20	16.4	78.1	644	6	US-09-925-065A-730267	Sequence 730267,
	21	16.4	78.1	1694	6	US-09-925-065A-90595	Sequence 90595, A
	22	16.4	78.1	1694	9	US-10-301-480-191836	Sequence 191836,
	23	16.4	78.1	1694	10	US-10-301-480-805245	Sequence 805245,
	24	16.4	78.1	2292	6	US-09-925-065A-549958	Sequence 549958,
	25	16.4	78.1	2292	10	US-10-301-480-527908	Sequence 527908,
	26	16.4	78.1	2292	10	US-10-301-480-1141317	Sequence 1141317,
	27	16.2	77.1	500	6	US-09-925-065A-617588	Sequence 617588,
c	28	16.2	77.1	522	6	US-09-925-065A-851205	Sequence 851205,
c	29	16.2	77.1	522	6	US-09-925-065A-851206	Sequence 851206,
	30	16.2	77.1	570	6	US-09-925-065A-796329	Sequence 796329,
	31	16.2	77.1	570	6	US-09-925-065A-796330	Sequence 796330,
	32	16.2	77.1	571	6	US-09-925-065A-163334	Sequence 163334,
	33	16.2	77.1	571	6	US-09-925-065A-163335	Sequence 163335,
	34	16.2	77.1	586	9	US-10-301-480-76571	Sequence 76571, A
	35	16.2	77.1	586	10	US-10-301-480-689980	Sequence 689980,
	36	16.2	77.1	603	10	US-10-301-480-255798	Sequence 255798,
	37	16.2	77.1	603	10	US-10-301-480-255799	Sequence 255799,
	38	16.2	77.1	603	10	US-10-301-480-869207	Sequence 869207,
	39	16.2	77.1	603	10	US-10-301-480-869208	Sequence 869208,
	40	16.2	77.1	611	6	US-09-925-065A-354220	Sequence 354220,
	41	16.2	77.1	620	10	US-10-301-480-425807	Sequence 425807,
	42	16.2	77.1	620	10	US-10-301-480-1039216	Sequence 1039216,
c	43	16.2	77.1	623	6	US-09-925-065A-622492	Sequence 622492,
c	44	16.2	77.1	623	6	US-09-925-065A-622493	Sequence 622493,
	45	16.2	77.1	625	10	US-10-301-480-567375	Sequence 567375,

ALIGNMENTS

RESULT 1
US-10-750-185-33312
; Sequence 33312, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 33312
; LENGTH: 3417
; TYPE: DNA
; ORGANISM: Bovine 19866880478621
US-10-750-185-33312

Query Match 84.8%; Score 17.8; DB 8; Length 3417;
Best Local Similarity 90.5%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 TGACTTGCCTAATTACCCTAA 21
              ||||||| ||||||| |||||
Db       3116 TGACTTGGCTAATTATCCTAA 3136
```

RESULT 2
US-10-750-623-33312
; Sequence 33312, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 24.483 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-8
Perfect score: 21
Sequence: 1 tgacttgcctaattaccctaa 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	8	US-10-677-254-8	Sequence 8, Appli
	2	21	100.0	21	8	US-10-717-573-8	Sequence 8, Appli
	3	21	100.0	435	8	US-10-677-254-1	Sequence 1, Appli
	4	21	100.0	435	8	US-10-717-573-1	Sequence 1, Appli
	5	21	100.0	480	8	US-10-677-254-30	Sequence 30, Appl
	6	21	100.0	480	8	US-10-717-573-30	Sequence 30, Appl
	7	21	100.0	2033	8	US-10-677-254-3	Sequence 3, Appli
	8	21	100.0	2033	8	US-10-717-573-3	Sequence 3, Appli
	9	21	100.0	2783	8	US-10-677-254-2	Sequence 2, Appli
	10	21	100.0	2783	8	US-10-717-573-2	Sequence 2, Appli
c	11	19.4	92.4	7495	7	US-10-742-828-5	Sequence 5, Appli
c	12	19.4	92.4	7508	7	US-10-742-828-4	Sequence 4, Appli
c	13	19.4	92.4	71843	9	US-10-488-292-3	Sequence 3, Appli
	14	17.8	84.8	13382	8	US-10-612-594-4	Sequence 4, Appli
c	15	17.8	84.8	3673778	6	US-10-312-841-1	Sequence 1, Appli
	16	17.4	82.9	1076	4	US-09-925-065A-699655	Sequence 699655,
	17	17.4	82.9	1076	4	US-09-925-065A-699656	Sequence 699656,
c	18	17	81.0	561	4	US-09-925-065A-346440	Sequence 346440,
	19	17	81.0	600	4	US-09-925-065A-729651	Sequence 729651,
c	20	17	81.0	606	4	US-09-925-065A-776627	Sequence 776627,
c	21	17	81.0	606	4	US-09-925-065A-776628	Sequence 776628,
	22	17	81.0	609	4	US-09-925-065A-763839	Sequence 763839,
	23	16.8	80.0	420	4	US-09-925-065A-656611	Sequence 656611,
	24	16.8	80.0	583	4	US-09-925-065A-375086	Sequence 375086,
c	25	16.8	80.0	317129	8	US-10-741-600-17765	Sequence 17765, A
	26	16.4	78.1	554	4	US-09-925-065A-652951	Sequence 652951,
	27	16.4	78.1	644	4	US-09-925-065A-730267	Sequence 730267,
	28	16.4	78.1	697	5	US-10-027-632-43982	Sequence 43982, A
	29	16.4	78.1	697	6	US-10-027-632-43982	Sequence 43982, A
	30	16.4	78.1	1694	4	US-09-925-065A-90595	Sequence 90595, A
	31	16.4	78.1	2292	4	US-09-925-065A-549958	Sequence 549958,
	32	16.4	78.1	5000	3	US-09-791-105-2	Sequence 2, Appli
c	33	16.4	78.1	6070	6	US-10-311-455-1652	Sequence 1652, Ap
c	34	16.4	78.1	6070	6	US-10-240-485-132	Sequence 132, App
c	35	16.4	78.1	6070	7	US-10-433-793-160	Sequence 160, App
c	36	16.4	78.1	7049	6	US-10-311-455-129	Sequence 129, App
c	37	16.4	78.1	7049	6	US-10-240-452-5	Sequence 5, Appli
c	38	16.4	78.1	10716	6	US-10-311-455-1391	Sequence 1391, Ap
c	39	16.4	78.1	33053	7	US-10-433-793-36	Sequence 36, Appl
c	40	16.4	78.1	37973	6	US-10-311-455-2169	Sequence 2169, Ap
c	41	16.4	78.1	73334	6	US-10-311-455-2098	Sequence 2098, Ap
c	42	16.4	78.1	73334	7	US-10-240-589C-128	Sequence 128, App
c	43	16.4	78.1	76798	3	US-09-880-107-3949	Sequence 3949, Ap
c	44	16.4	78.1	83391	7	US-10-433-793-123	Sequence 123, App
c	45	16.4	78.1	2140405	5	US-10-027-632-76212	Sequence 76212, A

ALIGNMENTS

RESULT 1
US-10-677-254-8
; Sequence 8, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-8

Query Match 100.0%; Score 21; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGACTTGCCTAATTACCCTAA 21
              |||||||||||||||||||||
Db          1 TGACTTGCCTAATTACCCTAA 21
```

RESULT 2
US-10-717-573-8
; Sequence 8, Application US/10717573
; Publication No. US20040209833A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/717,573
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 3.99328 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-7
Perfect score: 20
Sequence: 1 attttaagcaaacaaattaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	18.4	92.0	360	3	US-08-956-171E-3007	Sequence 3007, Ap
c	2	18.4	92.0	360	3	US-08-781-986A-3007	Sequence 3007, Ap
c	3	18.4	92.0	2854	3	US-08-936-165A-66	Sequence 66, Appl
c	4	18.4	92.0	3774	3	US-08-956-171E-660	Sequence 660, App
c	5	18.4	92.0	3774	3	US-08-781-986A-660	Sequence 660, App
c	6	17.4	87.0	360	3	US-09-270-767-8176	Sequence 8176, Ap
c	7	17.4	87.0	360	3	US-09-270-767-23458	Sequence 23458, A
c	8	17.4	87.0	601	3	US-09-949-016-120222	Sequence 120222,
c	9	17.4	87.0	84252	3	US-09-949-016-17315	Sequence 17315, A
	10	17.4	87.0	133063	3	US-09-949-016-16293	Sequence 16293, A
	11	17.4	87.0	219964	3	US-09-949-016-15086	Sequence 15086, A
c	12	17	85.0	712	3	US-09-463-239-3	Sequence 3, Appli
	13	16.8	84.0	2641	3	US-10-104-047-1176	Sequence 1176, Ap
c	14	16.8	84.0	3210	3	US-09-710-279-3922	Sequence 3922, Ap
	15	16.8	84.0	3254	3	US-09-710-279-4288	Sequence 4288, Ap
	16	16.8	84.0	3348	3	US-09-710-279-3732	Sequence 3732, Ap
c	17	16.8	84.0	3417	3	US-09-710-279-4318	Sequence 4318, Ap
c	18	16.8	84.0	4104	3	US-09-710-279-4107	Sequence 4107, Ap
c	19	16.8	84.0	9421	2	US-08-370-319C-2	Sequence 2, Appli
c	20	16.8	84.0	9421	3	US-09-224-834-2	Sequence 2, Appli
c	21	16.8	84.0	22914	3	US-09-949-016-12489	Sequence 12489, A
c	22	16.8	84.0	22914	3	US-09-949-016-15613	Sequence 15613, A
	23	16.8	84.0	23632	3	US-09-949-016-16270	Sequence 16270, A
c	24	16.8	84.0	25278	3	US-09-949-016-15913	Sequence 15913, A
	25	16.8	84.0	48920	3	US-09-949-016-11954	Sequence 11954, A
	26	16.8	84.0	51952	3	US-08-947-823-1	Sequence 1, Appli
	27	16.8	84.0	54576	3	US-09-949-016-15954	Sequence 15954, A
	28	16.8	84.0	54576	3	US-09-949-016-15955	Sequence 15955, A
c	29	16.8	84.0	60593	3	US-09-949-016-13779	Sequence 13779, A
c	30	16.8	84.0	76810	3	US-09-949-016-12528	Sequence 12528, A
	31	16.8	84.0	83462	3	US-09-949-016-15116	Sequence 15116, A
c	32	16.8	84.0	85368	3	US-09-949-016-12211	Sequence 12211, A
c	33	16.8	84.0	157032	3	US-09-949-016-16502	Sequence 16502, A
	34	16.8	84.0	194537	3	US-09-949-016-12928	Sequence 12928, A
	35	16.8	84.0	201529	3	US-09-949-016-12740	Sequence 12740, A
	36	16.8	84.0	373182	3	US-09-949-016-17371	Sequence 17371, A
	37	16.8	84.0	373694	3	US-09-949-016-12062	Sequence 12062, A
	38	16.8	84.0	1664976	3	US-08-916-421B-1	Sequence 1, Appli
c	39	16.8	84.0	1664976	3	US-08-916-421B-1	Sequence 1, Appli
	40	16.8	84.0	1664976	3	US-09-692-570-1	Sequence 1, Appli
c	41	16.8	84.0	1664976	3	US-09-692-570-1	Sequence 1, Appli
c	42	16.4	82.0	433	3	US-09-270-767-4014	Sequence 4014, Ap
c	43	16.4	82.0	433	3	US-09-270-767-19296	Sequence 19296, A
	44	16.4	82.0	601	3	US-09-949-016-85309	Sequence 85309, A
	45	16.4	82.0	601	3	US-09-949-016-206794	Sequence 206794,

ALIGNMENTS

```
RESULT 1
US-08-956-171E-3007/c
; Sequence 3007, Application US/08956171E
; Patent No. 6593114
;  GENERAL INFORMATION:
;       APPLICANT: Charles Kunsch
;                  Gil H. Choi
;                  Patrick S. Dillon
;                  Craig A. Rosen
;                  Steven C. Barash
;                  Michael R. Fannon
;       TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;       NUMBER OF SEQUENCES: 5256
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Human Genome Sciences, Inc.
;            STREET: 9410 Key West Avenue
;            CITY: Rockville
;            STATE: Maryland
;            COUNTRY: USA
;            ZIP: 20850
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;            COMPUTER: HP Vectra 486/33
;            OPERATING SYSTEM: MSDOS version 6.2
;            SOFTWARE: ASCII Text
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/956,171E
;            FILING DATE: 20-Oct-1997
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 60/009,861
;            FILING DATE: January 5, 1996
;            APPLICATION NUMBER: 08/781,986
;            FILING DATE: January 3, 1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Mark J. Hyman
;            REGISTRATION NUMBER: 46,789
;            REFERENCE/DOCKET NUMBER: PB248P1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (240) 314-1224
;            TELEFAX: (301) 309-8439
;  INFORMATION FOR SEQ ID NO: 3007:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 360 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 114.498 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-7
Perfect score: 20
Sequence: 1 attttaagcaaacaaattaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	606	9	BZ628666	BZ628666 ih61e11.g
c	2	20	100.0	658	10	CW316995	CW316995 104_808_1
	3	20	100.0	676	10	AG117483	AG117483 Pan_trog1
	4	19	95.0	370	6	CD737603	CD737603 4022963 1
c	5	19	95.0	443	6	CF431753	CF431753 NIT1_9_H1
c	6	19	95.0	460	2	BG411918	BG411918 OV2_39_G0
c	7	19	95.0	467	6	CA255060	CA255060 SCEPFL417
	8	19	95.0	490	10	CW452613	CW452613 fsbb001f1
	9	19	95.0	527	10	CL602277	CL602277 OB__Ba007
c	10	19	95.0	560	1	AJ750397	AJ750397 AJ750397
c	11	19	95.0	592	2	BE361833	BE361833 DG1_82_C0
	12	19	95.0	599	6	CA187197	CA187197 SCUTST308
c	13	19	95.0	603	2	BE361877	BE361877 DG1_82_G0
	14	19	95.0	605	3	BJ623706	BJ623706 BJ623706
	15	19	95.0	613	6	CA114220	CA114220 SCQSLB105
	16	19	95.0	632	10	CW302908	CW302908 104_787_1
	17	19	95.0	638	6	CA208660	CA208660 SCACSB111
	18	19	95.0	652	6	CA268391	CA268391 SCQSRT305
	19	19	95.0	773	10	CW782350	CW782350 OP__Ba007
	20	19	95.0	825	5	BU291905	BU291905 603606652
	21	19	95.0	871	10	CW525141	CW525141 OP__Ba004
	22	19	95.0	931	10	CW749813	CW749813 OP__Ba007
c	23	19	95.0	946	10	DU092949	DU092949 104490 To
	24	19	95.0	1453	8	DN714927	DN714927 CNB105-D0
c	25	18.4	92.0	169	9	BH617573	BH617573 SALK_0372
c	26	18.4	92.0	373	10	CG979574	CG979574 CH240_172
	27	18.4	92.0	436	11	DR25N8S	AL975961 Danio_rer
c	28	18.4	92.0	452	1	AI384587	AI384587 fb10g03.y
c	29	18.4	92.0	467	1	AJ625124	AJ625124 AJ625124
c	30	18.4	92.0	499	8	DN899017	DN899017 nap40c08.
c	31	18.4	92.0	520	11	DR14G24T	AL739217 Danio_rer
	32	18.4	92.0	532	10	BX229193	BX229193 Danio_rer
	33	18.4	92.0	553	10	CE644350	CE644350 tigr-gss-
c	34	18.4	92.0	559	9	BZ490173	BZ490173 BONO075TF
	35	18.4	92.0	567	8	DN896166	DN896166 nap06a06.
c	36	18.4	92.0	579	3	BM406069	BM406069 EST580396
c	37	18.4	92.0	580	10	CW599294	CW599294 OA_ABa013
	38	18.4	92.0	626	10	BX240255	BX240255 Danio_rer
c	39	18.4	92.0	636	11	DR43G11T	AL982510 Danio_rer
c	40	18.4	92.0	640	7	CO353502	CO353502 DR_ATE_FL
	41	18.4	92.0	659	9	AZ349621	AZ349621 1M0086M12
	42	18.4	92.0	673	7	CK680521	CK680521 ZF101-P00
c	43	18.4	92.0	687	10	BX197109	BX197109 Danio_rer
	44	18.4	92.0	699	9	AZ416632	AZ416632 1M0192P06
c	45	18.4	92.0	706	10	BX208190	BX208190 Danio_rer

ALIGNMENTS

RESULT 1
BZ628666
LOCUS BZ628666 606 bp DNA linear GSS 17-JAN-2003
DEFINITION ih61e11.g1 WGS-SbicolorF (DH5a methyl filtered) Sorghum bicolor genomic clone ih61e11 5', genomic survey sequence.
ACCESSION BZ628666
VERSION BZ628666.1 GI:27780751
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 606)
AUTHORS Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A.
TITLE Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
JOURNAL Unpublished (2002)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: ih61 row: e column: 11
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 606.
FEATURES Location/Qualifiers
source 1. .606
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="ih61e11"
/lab_host="DH5a"
/clone_lib="WGS-SbicolorF (DH5a methyl filtered)"
/note="Site_1: Xba I; Site_2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in M13mp19, .b/g reads in pUC19). The same ligation was transformed

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 16.3691 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-7
Perfect score: 20
Sequence: 1 attttaagcaaacaaattaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	13	ADT08248	Adt08248 Zebrafish
	2	20	100.0	20	13	ADT89056	Adt89056 Zebrafish
	3	20	100.0	435	13	ADT08242	Adt08242 Zebrafish
	4	20	100.0	435	13	ADT89050	Adt89050 Zebrafish
	5	20	100.0	480	13	ADT08271	Adt08271 Zebrafish
	6	20	100.0	480	13	ADT89079	Adt89079 Zebrafish
	7	20	100.0	2033	13	ADT08244	Adt08244 Zebrafish
	8	20	100.0	2033	13	ADT89052	Adt89052 Zebrafish
c	9	20	100.0	2766	6	ABZ70273	Abz70273 DNA polym
	10	20	100.0	2783	13	ADT08243	Adt08243 Zebrafish
	11	20	100.0	2783	13	ADT89051	Adt89051 Zebrafish
	12	20	100.0	2960	13	ADT89080	Adt89080 Zebrafish
c	13	18.4	92.0	360	2	AAV77318	Aav77318 Staphyloc
	14	18.4	92.0	1485	4	AAS52127	Aas52127 Staphyloc
	15	18.4	92.0	1539	4	AAS55190	Aas55190 Staphyloc
	16	18.4	92.0	1539	4	AAS54952	Aas54952 Staphyloc
	17	18.4	92.0	1539	8	ACA20111	Aca20111 Prokaryot
	18	18.4	92.0	1539	8	ACF74068	Acf74068 Staphyloc
c	19	18.4	92.0	2854	2	AAV53366	Aav53366 DNA encod
c	20	18.4	92.0	3774	2	AAV74971	Aav74971 Staphyloc
c	21	18	90.0	85548	13	ADV34999	Adv34999 Murine cD
c	22	17.4	87.0	473	6	ABA90463	Aba90463 Drosophil
c	23	17.4	87.0	473	6	ABA90465	Aba90465 Drosophil
	24	17.4	87.0	511	12	ADO85873	Ado85873 Exon 3 of
c	25	17.4	87.0	539	6	ABA90464	Aba90464 Drosophil
c	26	17.4	87.0	906	4	AAK80378	Aak80378 Human imm
c	27	17.4	87.0	906	4	AAK74454	Aak74454 Human imm
c	28	17.4	87.0	1933	6	ABZ57726	Abz57726 Human NAD
	29	17.4	87.0	3516	4	ABL29338	Abl29338 Drosophil
	30	17.4	87.0	3907	4	ABL29360	Abl29360 Drosophil
c	31	17.4	87.0	33632	4	ABL29040	Abl29040 Drosophil
c	32	17.4	87.0	37322	6	ABL61996	Abl61996 Colon ade
	33	17.4	87.0	104000	9	AAD57669	Aad57669 Human pho
	34	17	85.0	702	8	ACA30290	Aca30290 Prokaryot
c	35	17	85.0	712	2	AAX25080	Aax25080 Potato tu
	36	17	85.0	10200	4	AAK77727	Aak77727 Human imm
	37	17	85.0	154902	6	ABQ88198	Abq88198 Human ost
	38	16.8	84.0	107	2	AAQ77341	Aaq77341 Human gen
c	39	16.8	84.0	141	13	ADS04162	Ads04162 Staphyloc
	40	16.8	84.0	165	13	ADS04074	Ads04074 Staphyloc
	41	16.8	84.0	307	3	AAF18364	Aaf18364 Lung canc
c	42	16.8	84.0	462	4	AAK56918	Aak56918 Human imm
	43	16.8	84.0	534	5	ABV52288	Abv52288 Human pro
	44	16.8	84.0	549	3	AAC93993	Aac93993 Cat flea
	45	16.8	84.0	549	3	AAC94850	Aac94850 Cat flea

ALIGNMENTS

RESULT 1
ADT08248
ID ADT08248 standard; DNA; 20 BP.
XX
AC ADT08248;
XX
DT 13-JAN-2005 (first entry)
XX
DE Zebrafish L-FABP upstream region HNF-3beta binding site.
XX
KW Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer.
XX
OS Danio rerio.
XX
PN US2004209833-A1.
XX
PD 21-OCT-2004.
XX
PF 21-NOV-2003; 2003US-00717573.
XX
PR 16-APR-2003; 2003US-0463035P.
PR 27-MAY-2003; 2003US-0473210P.
XX
PA (WUJJ/) WU J.
PA (HERG/) HER G M.
XX
PI Wu J, Her GM;
XX
DR WPI; 2004-765481/75.
XX
PT New isolated polynucleotide useful for generating transgenic fish such as
PT zebrafish, comprises liver-specific expression control sequence that
PT modulates expression of vertebrate liver fatty acid binding protein.
XX
PS Claim 4; SEQ ID NO 7; 40pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a liver-
CC specific expression control sequence (LR) which modulates expression of a
CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 118.984 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-7
Perfect score: 20
Sequence: 1 attttaagcaaacaaattaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	2960	5	AF512998	AF512998 Danio rer
c	2	20	100.0	60709	14	AC107923	AC107923 Homo sapi
c	3	20	100.0	121952	14	AC151673	AC151673 Medicago
	4	20	100.0	121953	15	AC125481	AC125481 Medicago
	5	20	100.0	142257	5	BX005151	BX005151 Zebrafish
	6	20	100.0	151057	8	AC019198	AC019198 Homo sapi
	7	20	100.0	151397	14	CR792430	CR792430 Danio rer
c	8	20	100.0	154065	5	CR854838	CR854838 Zebrafish
	9	20	100.0	156578	14	CR786577	CR786577 Danio rer
	10	20	100.0	159188	5	CR381658	CR381658 Zebrafish
c	11	20	100.0	168663	8	AL354815	AL354815 Human DNA
c	12	20	100.0	176047	9	AC102338	AC102338 Mus muscu
c	13	20	100.0	178271	5	CR293507	CR293507 Zebrafish
c	14	20	100.0	184243	9	AC102296	AC102296 Mus muscu
c	15	19	95.0	169	10	AB150316	AB150316 Homo sapi
c	16	19	95.0	244	15	AY018859	AY018859 Oryza sat
	17	19	95.0	58009	14	AC087383	AC087383 Homo sapi
c	18	19	95.0	107758	14	CR925770	CR925770 Danio rer
c	19	19	95.0	110000	15	AP008211_033	Continuation (34 o
c	20	19	95.0	151235	8	AC090936	AC090936 Homo sapi
	21	19	95.0	159577	14	AC080060	AC080060 Homo sapi
c	22	19	95.0	160949	14	AC139622	AC139622 Danio rer
c	23	19	95.0	162088	14	AC069479	AC069479 Homo sapi
c	24	19	95.0	177153	15	AC119288	AC119288 Oryza sat
c	25	19	95.0	221511	5	CR391905	CR391905 Zebrafish
c	26	19	95.0	233137	14	AC094489	AC094489 Rattus no
	27	19	95.0	239843	14	AC115518	AC115518 Rattus no
c	28	18.4	92.0	360	6	AR356889	AR356889 Sequence
c	29	18.4	92.0	360	6	AR538445	AR538445 Sequence
c	30	18.4	92.0	791	10	BV641492	BV641492 S215P6173
	31	18.4	92.0	1539	6	AX620532	AX620532 Sequence
c	32	18.4	92.0	1605	5	BC095656	BC095656 Danio rer
	33	18.4	92.0	1821	2	AK114237	AK114237 Ciona int
c	34	18.4	92.0	2854	6	AR194517	AR194517 Sequence
c	35	18.4	92.0	3774	6	AR354542	AR354542 Sequence
c	36	18.4	92.0	3774	6	AR536098	AR536098 Sequence
	37	18.4	92.0	38279	8	AC127900	AC127900 Homo sapi
c	38	18.4	92.0	42644	5	CR627499	CR627499 Zebrafish
	39	18.4	92.0	60218	5	CR387987	CR387987 Zebrafish
	40	18.4	92.0	64183	14	AC164395	AC164395 Medicago
	41	18.4	92.0	65750	8	AC092542	AC092542 Homo sapi
	42	18.4	92.0	66694	5	BX908791	BX908791 Zebrafish
c	43	18.4	92.0	77143	5	BX927094	BX927094 Zebrafish
	44	18.4	92.0	80171	5	BX544872	BX544872 Zebrafish
c	45	18.4	92.0	80589	5	BX470257	BX470257 Zebrafish

ALIGNMENTS

RESULT 1
AF512998
LOCUS AF512998 2960 bp DNA linear VRT 10-JUL-2003
DEFINITION Danio rerio liver-type fatty acid binding protein gene, partial cds.
ACCESSION AF512998
VERSION AF512998.1 GI:21314558
KEYWORDS .
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 2960)
AUTHORS Her,G.M., Yeh,Y.H. and Wu,J.L.
TITLE 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish
JOURNAL Dev. Dyn. 227 (3), 347-356 (2003)
PUBMED 12815620
REFERENCE 2 (bases 1 to 2960)
AUTHORS Her,G.M. and Wu,J.-L.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chiu-Yuan Road, Sec. 2, Taipei 115, Taiwan
FEATURES Location/Qualifiers
source 1. .2960
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
mRNA <2784. .>2960
/product="liver-type fatty acid binding protein"
CDS 2784. .>2960
/note="Lfabp; small cytosolic protein involved in lipid transport and metabolism"
/codon_start=1
/product="liver-type fatty acid binding protein"
/protein_id="AAM47005.1"
/db_xref="GI:21314559"
/translation="MAFSGTWQVYAQENYEEFLRAISLPEEVIKLAKDVKPVTEIQQN GSDFTITSKTPGKTV"

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 17.7662 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-7
Perfect score: 20
Sequence: 1 attttaagcaaacaaattaa 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	18.4	92.0	529	10	US-10-301-480-486528	Sequence 486528,
c	2	18.4	92.0	529	10	US-10-301-480-1099937	Sequence 1099937,
c	3	18.4	92.0	531	6	US-09-925-065A-421812	Sequence 421812,
c	4	18.4	92.0	562	9	US-10-301-480-44854	Sequence 44854, A
c	5	18.4	92.0	562	10	US-10-301-480-658263	Sequence 658263,
	6	18.4	92.0	740	6	US-09-925-065A-820255	Sequence 820255,
c	7	18.4	92.0	186442	14	US-11-121-086-104	Sequence 104, App
c	8	17.4	87.0	487	6	US-09-925-065A-174746	Sequence 174746,
c	9	17.4	87.0	497	10	US-10-301-480-266137	Sequence 266137,
c	10	17.4	87.0	497	10	US-10-301-480-879546	Sequence 879546,
	11	17.4	87.0	575	6	US-09-925-065A-115209	Sequence 115209,
	12	17.4	87.0	581	9	US-10-301-480-214195	Sequence 214195,
	13	17.4	87.0	581	10	US-10-301-480-827604	Sequence 827604,
c	14	17.4	87.0	592	6	US-09-925-065A-159892	Sequence 159892,
c	15	17.4	87.0	593	10	US-10-301-480-252732	Sequence 252732,
c	16	17.4	87.0	593	10	US-10-301-480-866141	Sequence 866141,
c	17	17.4	87.0	620	6	US-09-925-065A-880084	Sequence 880084,
	18	17.4	87.0	626	6	US-09-925-065A-298915	Sequence 298915,
	19	17.4	87.0	627	10	US-10-301-480-375537	Sequence 375537,
	20	17.4	87.0	627	10	US-10-301-480-988946	Sequence 988946,
	21	17.4	87.0	998	10	US-10-301-480-595919	Sequence 595919,
	22	17.4	87.0	998	10	US-10-301-480-1209328	Sequence 1209328,
c	23	17.4	87.0	1203	9	US-10-301-480-29615	Sequence 29615, A
c	24	17.4	87.0	1203	10	US-10-301-480-643024	Sequence 643024,
	25	17.4	87.0	2022	8	US-10-750-185-37655	Sequence 37655, A
	26	17.4	87.0	2022	8	US-10-750-623-37655	Sequence 37655, A
c	27	17.4	87.0	3391	6	US-09-925-065A-711120	Sequence 711120,
c	28	17	85.0	538	6	US-09-925-065A-246840	Sequence 246840,
c	29	17	85.0	556	10	US-10-301-480-326998	Sequence 326998,
c	30	17	85.0	556	10	US-10-301-480-940407	Sequence 940407,
c	31	17	85.0	570	6	US-09-925-065A-787934	Sequence 787934,
c	32	17	85.0	613	6	US-09-925-065A-190239	Sequence 190239,
c	33	17	85.0	613	6	US-09-925-065A-190240	Sequence 190240,
c	34	17	85.0	617	10	US-10-301-480-279974	Sequence 279974,
c	35	17	85.0	617	10	US-10-301-480-279975	Sequence 279975,
c	36	17	85.0	617	10	US-10-301-480-893383	Sequence 893383,
c	37	17	85.0	617	10	US-10-301-480-893384	Sequence 893384,
	38	17	85.0	100000	14	US-11-124-367A-5091	Sequence 5091, Ap
	39	16.8	84.0	201	8	US-10-995-561-19356	Sequence 19356, A
c	40	16.8	84.0	436	9	US-10-301-480-3003	Sequence 3003, Ap
c	41	16.8	84.0	436	10	US-10-301-480-616412	Sequence 616412,
c	42	16.8	84.0	443	6	US-09-925-065A-617358	Sequence 617358,
c	43	16.8	84.0	477	6	US-09-925-065A-599889	Sequence 599889,
	44	16.8	84.0	491	6	US-09-925-065A-372151	Sequence 372151,
	45	16.8	84.0	502	9	US-10-301-480-3216	Sequence 3216, Ap

ALIGNMENTS

RESULT 1
US-10-301-480-486528/c
; Sequence 486528, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 486528
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-486528

Query Match 92.0%; Score 18.4; DB 10; Length 529;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATTTTAAGCAAACAAATTAA 20
              |||||||||| |||||||||
Db         41 ATTTTAAGCACACAAATTAA 22
```

RESULT 2
US-10-301-480-1099937/c
; Sequence 1099937, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 2.99496 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-6
Perfect score: 15
Sequence: 1 aatttatttgtgttg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	100.0	612	3	US-09-248-796A-1530	Sequence 1530, Ap
c	2	15	100.0	903	3	US-09-270-767-12919	Sequence 12919, A
c	3	15	100.0	2989	3	US-08-956-171E-150	Sequence 150, App
c	4	15	100.0	2989	3	US-08-781-986A-150	Sequence 150, App
	5	15	100.0	317366	3	US-09-949-016-16001	Sequence 16001, A
c	6	14	93.3	467	3	US-09-280-116-89	Sequence 89, Appl
c	7	14	93.3	601	3	US-09-949-016-53768	Sequence 53768, A
	8	14	93.3	601	3	US-09-949-016-143167	Sequence 143167,
c	9	14	93.3	601	3	US-09-949-016-144554	Sequence 144554,
c	10	14	93.3	601	3	US-09-949-016-144555	Sequence 144555,
c	11	14	93.3	686	3	US-09-270-767-5402	Sequence 5402, Ap
c	12	14	93.3	686	3	US-09-270-767-20684	Sequence 20684, A
c	13	14	93.3	2241	6	PCT-US95-10509-1	Sequence 1, Appli
	14	14	93.3	3517	3	US-10-104-047-647	Sequence 647, App
	15	14	93.3	3526	3	US-09-976-594-11	Sequence 11, Appl
	16	14	93.3	3680	3	US-09-647-390-15	Sequence 15, Appl
	17	14	93.3	6617	3	US-09-976-594-268	Sequence 268, App
c	18	14	93.3	12951	3	US-09-949-016-14075	Sequence 14075, A
	19	14	93.3	14759	3	US-09-661-887-1	Sequence 1, Appli
	20	14	93.3	15203	3	US-09-949-016-16410	Sequence 16410, A
c	21	14	93.3	17580	3	US-09-949-016-16055	Sequence 16055, A
	22	14	93.3	36075	3	US-09-949-016-16571	Sequence 16571, A
	23	14	93.3	36075	3	US-09-949-016-16572	Sequence 16572, A
	24	14	93.3	36625	3	US-09-949-016-12788	Sequence 12788, A
	25	14	93.3	37133	3	US-09-949-016-16569	Sequence 16569, A
	26	14	93.3	37133	3	US-09-949-016-16570	Sequence 16570, A
c	27	14	93.3	44393	3	US-09-949-016-14944	Sequence 14944, A
c	28	14	93.3	44393	3	US-09-949-016-14945	Sequence 14945, A
c	29	14	93.3	44393	3	US-09-949-016-14946	Sequence 14946, A
c	30	14	93.3	44393	3	US-09-949-016-16911	Sequence 16911, A
c	31	14	93.3	50563	3	US-09-949-016-15821	Sequence 15821, A
	32	14	93.3	69709	3	US-09-949-016-15784	Sequence 15784, A
	33	14	93.3	72662	3	US-09-949-016-17073	Sequence 17073, A
	34	14	93.3	78846	3	US-09-949-016-12396	Sequence 12396, A
	35	14	93.3	78846	3	US-09-949-016-12791	Sequence 12791, A
	36	14	93.3	78846	3	US-09-949-016-12792	Sequence 12792, A
	37	14	93.3	78846	3	US-09-949-016-12793	Sequence 12793, A
	38	14	93.3	78850	3	US-09-949-016-16013	Sequence 16013, A
	39	14	93.3	78850	3	US-09-949-016-16014	Sequence 16014, A
	40	14	93.3	78850	3	US-09-949-016-16015	Sequence 16015, A
	41	14	93.3	78850	3	US-09-949-016-16016	Sequence 16016, A
	42	14	93.3	78850	3	US-09-949-016-16201	Sequence 16201, A
	43	14	93.3	78850	3	US-09-949-016-16202	Sequence 16202, A
	44	14	93.3	78850	3	US-09-949-016-16203	Sequence 16203, A
	45	14	93.3	78850	3	US-09-949-016-16204	Sequence 16204, A

ALIGNMENTS

RESULT 1
US-09-248-796A-1530/c
; Sequence 1530, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1530
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1530

Query Match 100.0%; Score 15; DB 3; Length 612;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AATTTATTTGTGTTG 15
              |||||||||||||||
Db         20 AATTTATTTGTGTTG 6
```

RESULT 2
US-09-270-767-12919/c
; Sequence 12919, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12919
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Drosophila melanogaster

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 85.8732 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-6
Perfect score: 15
Sequence: 1 aatttatttgtgttg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		15	100.0	86	7	CN872089	CN872089 010211AAP
2	c	15	100.0	137	3	BI324061	BI324061 kt53a03.y
3		15	100.0	161	10	BX124334	BX124334 Danio rer
4	c	15	100.0	163	1	AW522511	AW522511 UI-R-BO0-
5	c	15	100.0	183	10	CZ365564	CZ365564 ZMMBF0145
6		15	100.0	183	10	BX190591	BX190591 Danio rer
7		15	100.0	185	9	CC095316	CC095316 CSU-K34.1
8	c	15	100.0	216	9	CC970346	CC970346 ZUAFD88TV
9	c	15	100.0	217	9	CC746949	CC746949 ZMMBBb012
10		15	100.0	234	1	AV240038	AV240038 AV240038
11	c	15	100.0	248	10	CG408145	CG408145 ZMMBBb028
12	c	15	100.0	252	10	CL446525	CL446525 ZMMBBb046
13		15	100.0	254	9	CC676891	CC676891 OGUIR05TH
14	c	15	100.0	278	10	CG904523	CG904523 ZMMBBb051
15		15	100.0	280	2	BB410707	BB410707 BB410707
16	c	15	100.0	284	10	CG091693	CG091693 PUKCX01TB
17	c	15	100.0	286	10	CL226055	CL226055 ZMMBBc057
18		15	100.0	289	10	CG091695	CG091695 PUKCX01TD
19		15	100.0	295	9	CE238834	CE238834 tigr-gss-
20	c	15	100.0	313	8	T01835	T01835 wEST02556 E
21		15	100.0	313	10	CG720870	CG720870 1119064C1
22	c	15	100.0	322	10	CL449105	CL449105 ZMMBBb046
23	c	15	100.0	324	9	CC787357	CC787357 ZMMBBb015
24		15	100.0	327	10	CG873320	CG873320 ZMMBBc028
25	c	15	100.0	333	1	AW165275	AW165275 fe06h07.x
26	c	15	100.0	338	2	BG301524	BG301524 kt02b09.y
27	c	15	100.0	341	2	BG301665	BG301665 kt03h12.y
28		15	100.0	341	7	CV475153	CV475153 23648.1 D
29		15	100.0	344	10	BX157285	BX157285 Danio rer
30	c	15	100.0	346	9	CC761571	CC761571 ZMMBBb021
31	c	15	100.0	347	2	BG301417	BG301417 kt04b02.y
32		15	100.0	348	5	BY577034	BY577034 BY577034
33		15	100.0	351	9	CC382054	CC382054 PUHKD05TB
34	c	15	100.0	352	2	BG301541	BG301541 kt02d03.y
35		15	100.0	356	10	CG422080	CG422080 ZMMBBc003
36	c	15	100.0	357	2	BG301903	BG301903 kt07a01.y
37		15	100.0	357	10	CG876818	CG876818 ZMMBBc028
38	c	15	100.0	362	5	BQ479395	BQ479395 ku35b03.y
39		15	100.0	367	10	CG994153	CG994153 ZMMBBb037
40	c	15	100.0	376	10	CG915201	CG915201 ZMMBBb038
41	c	15	100.0	381	2	BG301858	BG301858 kt06c09.y
42	c	15	100.0	384	10	CL395037	CL395037 ZMMBBb021
43		15	100.0	385	9	AQ023189	AQ023189 HS_2177_B
44	c	15	100.0	396	2	BG301349	BG301349 kt04c11.y
45	c	15	100.0	397	7	CR419357	CR419357 CR419357

ALIGNMENTS

RESULT 1
CN872089
LOCUS CN872089 86 bp mRNA linear EST 04-JUN-2004
DEFINITION 010211AAPA002796HT (AAPA) Royal Gala 24 DAFB fruit Malus x domestica cDNA clone AAPA002796, mRNA sequence.
ACCESSION CN872089
VERSION CN872089.1 GI:48258247
KEYWORDS EST.
SOURCE Malus x domestica
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
REFERENCE 1 (bases 1 to 86)
AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
TITLE HortResearch Apple EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Gleave,A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
FEATURES Location/Qualifiers
source 1. .86
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAPA002796"
/tissue_type="Fruit"
/dev_stage="24 days after full bloom"
/clone_lib="(AAPA) Royal Gala 24 DAFB fruit"
/note="Vector: pBK-CMV; Library sequenced by Genesis Research & Development"
ORIGIN

Query Match 100.0%; Score 15; DB 7; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTTATTTGTGTTG 15
||||||||||||||||
Db 53 AATTTATTTGTGTTG 67

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 12.2768 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-6
Perfect score: 15
Sequence: 1 aatttatttgtgttg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		15	100.0	15	13	ADT08247	Adt08247 Zebrafish
2		15	100.0	15	13	ADT89055	Adt89055 Zebrafish
3	c	15	100.0	201	13	ADS39920	Ads39920 Human aut
4		15	100.0	315	8	ACF75120	Acf75120 Staphyloc
5		15	100.0	435	13	ADT08242	Adt08242 Zebrafish
6		15	100.0	435	13	ADT89050	Adt89050 Zebrafish
7		15	100.0	480	13	ADT08271	Adt08271 Zebrafish
8		15	100.0	480	13	ADT89079	Adt89079 Zebrafish
9		15	100.0	501	3	AAA45092	Aaa45092 Human sec
10		15	100.0	554	6	ABQ27596	Abq27596 Oligonucl
11	c	15	100.0	554	6	ABQ27597	Abq27597 Oligonucl
12		15	100.0	555	6	ABQ33730	Abq33730 Oligonucl
13	c	15	100.0	555	6	ABQ33731	Abq33731 Oligonucl
14		15	100.0	733	13	ADR61902	Adr61902 Cotton cD
15		15	100.0	2033	13	ADT08244	Adt08244 Zebrafish
16		15	100.0	2033	13	ADT89052	Adt89052 Zebrafish
17		15	100.0	2783	13	ADT08243	Adt08243 Zebrafish
18		15	100.0	2783	13	ADT89051	Adt89051 Zebrafish
19		15	100.0	2960	13	ADT89080	Adt89080 Zebrafish
20	c	15	100.0	2989	2	AAV74461	Aav74461 Staphyloc
21		15	100.0	4110	4	ABL07042	Abl07042 Drosophil
22		15	100.0	4986	4	AAL05843	Aal05843 Human rep
23		15	100.0	4986	4	ABL98407	Abl98407 Human tes
24		15	100.0	5146	10	ADD48890	Add48890 Human gen
25		15	100.0	5542	6	ABL34021	Abl34021 Human imm
26		15	100.0	6197	6	ABL33711	Abl33711 Human imm
27		15	100.0	6436	6	ABL32681	Abl32681 Human imm
28	c	15	100.0	11806	8	ACA22763	Aca22763 Prokaryot
29		15	100.0	14598	4	AAK80690	Aak80690 Human imm
30		15	100.0	14598	4	AAK79627	Aak79627 Human imm
31	c	15	100.0	110000	6	ABQ67196_5	Continuation (6 of
32		15	100.0	110000	6	ABQ69245_27	Continuation (28 o
33	c	15	100.0	110000	8	ABX16390_0	Abx16390 Mouse hig
34		15	100.0	110000	12	ADO34435_5	Continuation (6 of
35	c	15	100.0	154799	13	ADS36467	Ads36467 Human aut
36	c	15	100.0	235962	14	ADZ12926	Adz12926 Murine ca
37	c	14	93.3	41	6	ABZ49694	Abz49694 Human sul
38	c	14	93.3	41	6	ABZ43541	Abz43541 Human sul
39	c	14	93.3	49	8	ACC00253	Acc00253 rapL gene
40		14	93.3	50	8	ACC00242	Acc00242 rapL gene
41		14	93.3	141	12	ADG99575	Adg99575 Kidney di
42		14	93.3	266	2	AAQ77295	Aaq77295 Human gen
43	c	14	93.3	380	6	ABL64512	Abl64512 Stomach c
44	c	14	93.3	380	6	ABL67566	Abl67566 Oesophagu
45		14	93.3	395	4	AAL00951	Aal00951 Human rep

ALIGNMENTS

RESULT 1
ADT08247
ID ADT08247 standard; DNA; 15 BP.
XX
AC ADT08247;
XX
DT 13-JAN-2005 (first entry)
XX
DE Zebrafish L-FABP upstream region HNF-1alpha binding site.
XX
KW Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer.
XX
OS Danio rerio.
XX
PN US2004209833-A1.
XX
PD 21-OCT-2004.
XX
PF 21-NOV-2003; 2003US-00717573.
XX
PR 16-APR-2003; 2003US-0463035P.
PR 27-MAY-2003; 2003US-0473210P.
XX
PA (WUJJ/) WU J.
PA (HERG/) HER G M.
XX
PI Wu J, Her GM;
XX
DR WPI; 2004-765481/75.
XX
PT New isolated polynucleotide useful for generating transgenic fish such as
PT zebrafish, comprises liver-specific expression control sequence that
PT modulates expression of vertebrate liver fatty acid binding protein.
XX
PS Claim 4; SEQ ID NO 6; 40pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a liver-
CC specific expression control sequence (LR) which modulates expression of a
CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 89.238 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-6
Perfect score: 15
Sequence: 1 aatttatttgtgttg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	100.0	201	6	CQ930101	CQ930101 Sequence
c	2	15	100.0	314	10	AU026431	AU026431 Rattus no
	3	15	100.0	315	6	AX622636	AX622636 Sequence
	4	15	100.0	486	10	BV165522	BV165522 PNDKN1-1
	5	15	100.0	486	10	BV165523	BV165523 PNDKN1-2
	6	15	100.0	500	2	CEDAD1	X89080 C.elegans d
c	7	15	100.0	570	13	AY136052	AY136052 HIV-1 iso
c	8	15	100.0	570	13	AY136070	AY136070 HIV-1 iso
	9	15	100.0	592	10	BV677735	BV677735 ST18_2399
c	10	15	100.0	612	6	AR546399	AR546399 Sequence
	11	15	100.0	630	10	BV257210	BV257210 S235P6526
	12	15	100.0	669	8	HSA332937	AJ332937 Homo sapi
	13	15	100.0	698	10	BV594471	BV594471 S215P6832
	14	15	100.0	756	10	BV618937	BV618937 S215P6892
c	15	15	100.0	903	6	AR507959	AR507959 Sequence
	16	15	100.0	945	10	BV466903	BV466903 G591P6326
	17	15	100.0	1373	2	AY161297	AY161297 Cystidico
	18	15	100.0	1376	2	AY161296	AY161296 Cystidico
	19	15	100.0	1533	2	AF251548	AF251548 Tribolium
	20	15	100.0	1605	5	BC095656	BC095656 Danio rer
	21	15	100.0	2960	5	AF512998	AF512998 Danio rer
c	22	15	100.0	2989	6	AR354032	AR354032 Sequence
c	23	15	100.0	2989	6	AR535588	AR535588 Sequence
	24	15	100.0	3227	2	BT003585	BT003585 Drosophil
	25	15	100.0	4110	6	CQ580046	CQ580046 Sequence
	26	15	100.0	4778	2	AY699069	AY699069 Haemonchu
	27	15	100.0	5542	6	AX346923	AX346923 Sequence
	28	15	100.0	6197	6	AX346613	AX346613 Sequence
	29	15	100.0	6308	6	CS114271	CS114271 Sequence
	30	15	100.0	6308	6	CS114295	CS114295 Sequence
	31	15	100.0	6436	6	AX345583	AX345583 Sequence
	32	15	100.0	7515	5	BX908746	BX908746 Zebrafish
c	33	15	100.0	10368	5	BX908781	BX908781 Zebrafish
	34	15	100.0	11784	2	AY337337	AY337337 Tribolium
c	35	15	100.0	12445	5	CR936480	CR936480 Zebrafish
	36	15	100.0	16703	2	AY699067	AY699067 Haemonchu
c	37	15	100.0	19722	5	AL935210	AL935210 Zebrafish
c	38	15	100.0	22512	5	CR812483	CR812483 Zebrafish
c	39	15	100.0	27213	8	AP000291	AP000291 Homo sapi
	40	15	100.0	29075	14	AC020390	AC020390 Drosophil
	41	15	100.0	35390	5	CR936413	CR936413 Zebrafish
c	42	15	100.0	35484	2	CET26E4	Z81132 Caenorhabdi
c	43	15	100.0	35729	5	AC144704	AC144704 Danio rer
c	44	15	100.0	36296	2	AF039713	AF039713 Caenorhab
	45	15	100.0	37798	14	AC146501	AC146501 Danio rer

ALIGNMENTS

RESULT 1
CQ930101/c
LOCUS CQ930101 201 bp DNA linear PAT 23-NOV-2004
DEFINITION Sequence 5134 from Patent WO2004083403.
ACCESSION CQ930101
VERSION CQ930101.1 GI:56219491
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Cargill,M., Begovich,A.B. and Alexander,H.C.
TITLE Genetic polymorphisms associated with rheumatoid arthritis, methods of detection and uses thereof
JOURNAL Patent: WO 2004083403-A 5134 30-SEP-2004;
Applera Corporation (US)
FEATURES Location/Qualifiers
source 1. .201
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTTATTTGTGTTG 15
||||||||||||||
Db 198 AATTTATTTGTGTTG 184

RESULT 2
AU026431/c
LOCUS AU026431 314 bp DNA linear STS 02-MAR-1999
DEFINITION Rattus norvegicus, OTSUKA clone, OT54.09/954c07, microsatellite sequence, sequence tagged site.
ACCESSION AU026431
VERSION AU026431.1 GI:4516354

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 13.3246 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-6
Perfect score: 15
Sequence: 1 aatttatttgtgttg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	15	100.0	248	14	US-11-128-061-5461	Sequence 5461, Ap
c 2	15	100.0	248	14	US-11-128-049-5461	Sequence 5461, Ap
c 3	15	100.0	269	14	US-11-128-061-1819	Sequence 1819, Ap
c 4	15	100.0	269	14	US-11-128-049-1819	Sequence 1819, Ap
c 5	15	100.0	382	10	US-10-301-480-415673	Sequence 415673,
c 6	15	100.0	382	10	US-10-301-480-1029082	Sequence 1029082,
c 7	15	100.0	389	6	US-09-925-065A-342955	Sequence 342955,
c 8	15	100.0	508	6	US-09-925-065A-325416	Sequence 325416,
c 9	15	100.0	508	6	US-09-925-065A-325417	Sequence 325417,
c 10	15	100.0	508	6	US-09-925-065A-325418	Sequence 325418,
c 11	15	100.0	508	6	US-09-925-065A-325419	Sequence 325419,
c 12	15	100.0	526	10	US-10-301-480-399708	Sequence 399708,
c 13	15	100.0	526	10	US-10-301-480-399709	Sequence 399709,
c 14	15	100.0	526	10	US-10-301-480-399710	Sequence 399710,
c 15	15	100.0	526	10	US-10-301-480-399711	Sequence 399711,
c 16	15	100.0	526	10	US-10-301-480-1013117	Sequence 1013117,
c 17	15	100.0	526	10	US-10-301-480-1013118	Sequence 1013118,
c 18	15	100.0	526	10	US-10-301-480-1013119	Sequence 1013119,
c 19	15	100.0	526	10	US-10-301-480-1013120	Sequence 1013120,
c 20	15	100.0	540	6	US-09-925-065A-342956	Sequence 342956,
c 21	15	100.0	545	10	US-10-301-480-415674	Sequence 415674,
c 22	15	100.0	545	10	US-10-301-480-1029083	Sequence 1029083,
23	15	100.0	553	9	US-10-301-480-4386	Sequence 4386, Ap
24	15	100.0	553	10	US-10-301-480-617795	Sequence 617795,
c 25	15	100.0	563	6	US-09-925-065A-164580	Sequence 164580,
c 26	15	100.0	586	10	US-10-301-480-256922	Sequence 256922,
c 27	15	100.0	586	10	US-10-301-480-870331	Sequence 870331,
c 28	15	100.0	593	6	US-09-925-065A-28868	Sequence 28868, A
c 29	15	100.0	593	9	US-10-301-480-130106	Sequence 130106,
c 30	15	100.0	593	10	US-10-301-480-743515	Sequence 743515,
31	15	100.0	604	6	US-09-925-065A-581603	Sequence 581603,
32	15	100.0	604	6	US-09-925-065A-581604	Sequence 581604,
33	15	100.0	615	6	US-09-925-065A-531920	Sequence 531920,
c 34	15	100.0	617	6	US-09-925-065A-138293	Sequence 138293,
c 35	15	100.0	620	10	US-10-301-480-233560	Sequence 233560,
c 36	15	100.0	620	10	US-10-301-480-846969	Sequence 846969,
c 37	15	100.0	645	6	US-09-925-065A-819884	Sequence 819884,
c 38	15	100.0	647	6	US-09-925-065A-915865	Sequence 915865,
c 39	15	100.0	675	6	US-09-925-065A-899678	Sequence 899678,
c 40	15	100.0	694	6	US-09-925-065A-548225	Sequence 548225,
c 41	15	100.0	694	6	US-09-925-065A-548226	Sequence 548226,
c 42	15	100.0	694	6	US-09-925-065A-548227	Sequence 548227,
c 43	15	100.0	694	6	US-09-925-065A-548228	Sequence 548228,
c 44	15	100.0	694	6	US-09-925-065A-548229	Sequence 548229,
c 45	15	100.0	694	10	US-10-301-480-526175	Sequence 526175,

ALIGNMENTS

RESULT 1
US-11-128-061-5461/c
; Sequence 5461, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5461
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-5461

Query Match 100.0%; Score 15; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AATTTATTTGTGTTG 15
              |||||||||||||||
Db        152 AATTTATTTGTGTTG 138
```

RESULT 2
US-11-128-049-5461/c
; Sequence 5461, Application US/11128049
; Publication No. US20060010513A1

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 17.4879 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-6
Perfect score: 15
Sequence: 1 aatttatttgtgttg 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		15	100.0	15	8	US-10-677-254-6	Sequence 6, Appli
2		15	100.0	15	8	US-10-717-573-6	Sequence 6, Appli
3	c	15	100.0	389	4	US-09-925-065A-342955	Sequence 342955,
4		15	100.0	435	8	US-10-677-254-1	Sequence 1, Appli
5		15	100.0	435	8	US-10-717-573-1	Sequence 1, Appli
6		15	100.0	480	8	US-10-677-254-30	Sequence 30, Appl
7		15	100.0	480	8	US-10-717-573-30	Sequence 30, Appl
8	c	15	100.0	508	4	US-09-925-065A-325416	Sequence 325416,
9	c	15	100.0	508	4	US-09-925-065A-325417	Sequence 325417,
10	c	15	100.0	508	4	US-09-925-065A-325418	Sequence 325418,
11	c	15	100.0	508	4	US-09-925-065A-325419	Sequence 325419,
12	c	15	100.0	540	4	US-09-925-065A-342956	Sequence 342956,
13		15	100.0	554	8	US-10-363-345A-14187	Sequence 14187, A
14	c	15	100.0	554	8	US-10-363-345A-14188	Sequence 14188, A
15		15	100.0	554	9	US-10-363-483A-14187	Sequence 14187, A
16	c	15	100.0	554	9	US-10-363-483A-14188	Sequence 14188, A
17		15	100.0	555	8	US-10-363-345A-20321	Sequence 20321, A
18	c	15	100.0	555	8	US-10-363-345A-20322	Sequence 20322, A
19		15	100.0	555	9	US-10-363-483A-20321	Sequence 20321, A
20	c	15	100.0	555	9	US-10-363-483A-20322	Sequence 20322, A
21	c	15	100.0	563	4	US-09-925-065A-164580	Sequence 164580,
22	c	15	100.0	570	5	US-10-027-632-45494	Sequence 45494, A
23	c	15	100.0	570	6	US-10-027-632-45494	Sequence 45494, A
24	c	15	100.0	579	5	US-10-027-632-3137	Sequence 3137, Ap
25	c	15	100.0	579	6	US-10-027-632-3137	Sequence 3137, Ap
26	c	15	100.0	581	5	US-10-027-632-59922	Sequence 59922, A
27	c	15	100.0	581	5	US-10-027-632-60653	Sequence 60653, A
28	c	15	100.0	581	5	US-10-027-632-60896	Sequence 60896, A
29	c	15	100.0	581	5	US-10-027-632-298492	Sequence 298492,
30	c	15	100.0	581	6	US-10-027-632-59922	Sequence 59922, A
31	c	15	100.0	581	6	US-10-027-632-60653	Sequence 60653, A
32	c	15	100.0	581	6	US-10-027-632-60896	Sequence 60896, A
33	c	15	100.0	581	6	US-10-027-632-298492	Sequence 298492,
34		15	100.0	581	7	US-10-767-701-31491	Sequence 31491, A
35	c	15	100.0	593	4	US-09-925-065A-28868	Sequence 28868, A
36		15	100.0	604	4	US-09-925-065A-581603	Sequence 581603,
37		15	100.0	604	4	US-09-925-065A-581604	Sequence 581604,
38		15	100.0	615	4	US-09-925-065A-531920	Sequence 531920,
39	c	15	100.0	617	4	US-09-925-065A-138293	Sequence 138293,
40	c	15	100.0	645	4	US-09-925-065A-819884	Sequence 819884,
41	c	15	100.0	647	4	US-09-925-065A-915865	Sequence 915865,
42	c	15	100.0	675	4	US-09-925-065A-899678	Sequence 899678,
43	c	15	100.0	694	4	US-09-925-065A-548225	Sequence 548225,
44	c	15	100.0	694	4	US-09-925-065A-548226	Sequence 548226,
45	c	15	100.0	694	4	US-09-925-065A-548227	Sequence 548227,

ALIGNMENTS

RESULT 1
US-10-677-254-6
; Sequence 6, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-6

Query Match 100.0%; Score 15; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTTATTTGTGTTG 15
||||||||||||||| |
Db 1 AATTTATTTGTGTTG 15

RESULT 2
US-10-717-573-6
; Sequence 6, Application US/10717573
; Publication No. US20040209833A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/717,573
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 15
; TYPE: DNA

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 2.59563 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-5
Perfect score: 13
Sequence: 1 aaaataaacaggg 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	13	100.0	204	3	US-09-248-796A-8945	Sequence 8945, Ap
2	13	100.0	279	3	US-09-134-000C-1864	Sequence 1864, Ap
3	13	100.0	299	3	US-09-270-767-27951	Sequence 27951, A
4	13	100.0	362	3	US-09-270-767-6589	Sequence 6589, Ap
5	13	100.0	362	3	US-09-270-767-21871	Sequence 21871, A
6	13	100.0	503	3	US-09-621-976-14126	Sequence 14126, A
7	13	100.0	601	3	US-09-949-016-32072	Sequence 32072, A
8	13	100.0	601	3	US-09-949-016-32073	Sequence 32073, A
c 9	13	100.0	601	3	US-09-949-016-45032	Sequence 45032, A
10	13	100.0	601	3	US-09-949-016-70051	Sequence 70051, A
11	13	100.0	601	3	US-09-949-016-76914	Sequence 76914, A
c 12	13	100.0	601	3	US-09-949-016-84047	Sequence 84047, A
c 13	13	100.0	601	3	US-09-949-016-84048	Sequence 84048, A
c 14	13	100.0	601	3	US-09-949-016-110804	Sequence 110804,
c 15	13	100.0	601	3	US-09-949-016-110965	Sequence 110965,
c 16	13	100.0	601	3	US-09-949-016-111126	Sequence 111126,
c 17	13	100.0	601	3	US-09-949-016-111287	Sequence 111287,
18	13	100.0	601	3	US-09-949-016-129025	Sequence 129025,
19	13	100.0	601	3	US-09-949-016-129026	Sequence 129026,
20	13	100.0	601	3	US-09-949-016-142486	Sequence 142486,
21	13	100.0	601	3	US-09-949-016-178033	Sequence 178033,
22	13	100.0	601	3	US-09-949-016-178034	Sequence 178034,
23	13	100.0	601	3	US-09-949-016-189483	Sequence 189483,
c 24	13	100.0	601	3	US-09-949-016-201247	Sequence 201247,
c 25	13	100.0	601	3	US-09-949-016-201361	Sequence 201361,
c 26	13	100.0	736	3	US-09-270-767-10249	Sequence 10249, A
27	13	100.0	825	3	US-09-270-767-12216	Sequence 12216, A
c 28	13	100.0	965	3	US-09-270-767-9078	Sequence 9078, Ap
c 29	13	100.0	965	3	US-09-270-767-24360	Sequence 24360, A
c 30	13	100.0	1693	3	US-09-149-476-224	Sequence 224, App
c 31	13	100.0	1753	3	US-09-149-476-56	Sequence 56, Appl
32	13	100.0	12311	3	US-08-750-717-1	Sequence 1, Appli
c 33	13	100.0	15379	3	US-09-949-016-14191	Sequence 14191, A
c 34	13	100.0	20634	3	US-09-949-016-16627	Sequence 16627, A
35	13	100.0	32868	3	US-09-949-016-17406	Sequence 17406, A
36	13	100.0	33519	3	US-09-949-016-17165	Sequence 17165, A
37	13	100.0	37385	3	US-09-949-016-12466	Sequence 12466, A
38	13	100.0	37388	3	US-09-949-016-16846	Sequence 16846, A
39	13	100.0	56551	3	US-09-949-016-12030	Sequence 12030, A
40	13	100.0	83851	3	US-09-949-016-13847	Sequence 13847, A
41	13	100.0	86956	3	US-09-949-016-12994	Sequence 12994, A
42	13	100.0	105050	3	US-09-949-016-15953	Sequence 15953, A
43	13	100.0	118999	3	US-09-791-105B-32	Sequence 32, Appl
c 44	13	100.0	118999	3	US-09-791-105B-32	Sequence 32, Appl
45	13	100.0	134890	3	US-09-949-016-15602	Sequence 15602, A

ALIGNMENTS

RESULT 1
US-09-248-796A-8945/c
; Sequence 8945, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAI
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 8945
; LENGTH: 204
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-8945

Query Match 100.0%; Score 13; DB 3; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AAAATAAACAGGG 13
              |||||||||||||
Db        186 AAAATAAACAGGG 174
```

RESULT 2
US-09-134-000C-1864
; Sequence 1864, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1864

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 74.4234 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-5
Perfect score: 13
Sequence: 1 aaaataaacaggg 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	100.0	56	10	BX153895	BX153895 Danio rer
c 2	13	100.0	92	6	CF554321	CF554321 SSHGgW69
c 3	13	100.0	94	7	CN868582	CN868582 001116AAO
4	13	100.0	102	1	AW933765	AW933765 EST359608
5	13	100.0	115	9	AQ925602	AQ925602 RPCI-23-2
6	13	100.0	131	1	AI705517	AI705517 UI-R-AC1-
7	13	100.0	131	9	AQ372908	AQ372908 RPCI11-15
c 8	13	100.0	135	1	AA254394	AA254394 va15h03.r
9	13	100.0	139	3	BJ252096	BJ252096 BJ252096
c 10	13	100.0	143	9	AZ447880	AZ447880 1M0245D17
11	13	100.0	147	11	DR37D7S	AL984919 Danio rer
c 12	13	100.0	148	11	DR32D4S	AL973819 Danio rer
c 13	13	100.0	150	9	BH291577	BH291577 CH230-114
14	13	100.0	155	10	CG786368	CG786368 ZMMBBb011
15	13	100.0	156	3	BM327327	BM327327 PIC1_12_B
16	13	100.0	160	10	AG023082	AG023082 Oryza sat
17	13	100.0	161	3	BI631314	BI631314 RH60867.5
c 18	13	100.0	162	9	BH116400	BH116400 RPCI-24-3
c 19	13	100.0	163	9	BH327180	BH327180 CH230-116
c 20	13	100.0	166	1	AL387438	AL387438 MtBC42E10
c 21	13	100.0	168	2	BI075074	BI075074 IP1_20_D0
22	13	100.0	168	9	AZ893740	AZ893740 RPCI-24-1
23	13	100.0	172	3	BM660685	BM660685 952040H09
24	13	100.0	174	9	CC022348	CC022348 3591_1_29
25	13	100.0	176	1	AI065778	AI065778 ag93b04.x
c 26	13	100.0	177	5	BQ905285	BQ905285 Ta04_13e1
27	13	100.0	180	1	AJ485048	AJ485048 AJ485048
28	13	100.0	181	2	BB571970	BB571970 BB571970
c 29	13	100.0	187	6	CD938893	CD938893 OV.111G05
30	13	100.0	188	9	AQ985956	AQ985956 RPCI-23-3
c 31	13	100.0	188	9	CE143506	CE143506 tigr-gss-
c 32	13	100.0	191	7	CK107033	CK107033 UB44DPA10
c 33	13	100.0	191	7	CO541293	CO541293 Mdfrt3039
c 34	13	100.0	192	2	BF360687	BF360687 QV4-OT003
35	13	100.0	192	2	BF990690	BF990690 RC6-GN007
c 36	13	100.0	192	11	DR30F18T	AL736750 Danio rer
37	13	100.0	197	6	CB434762	CB434762 611431 MA
c 38	13	100.0	198	1	AV303123	AV303123 AV303123
c 39	13	100.0	198	2	BF368815	BF368815 RC6-GN007
40	13	100.0	198	2	BI035678	BI035678 PM2-NN016
c 41	13	100.0	199	10	BX653439	BX653439 Arabidops
c 42	13	100.0	201	6	CD929958	CD929958 GR45.109K
c 43	13	100.0	202	1	AV114315	AV114315 AV114315
44	13	100.0	205	1	AI033978	AI033978 ow13a01.x
c 45	13	100.0	206	2	BG004275	BG004275 RC6-GN007

ALIGNMENTS

RESULT 1
BX153895
LOCUS BX153895 56 bp DNA linear GSS 28-JAN-2003
DEFINITION Danio rerio genomic clone DKEY-116L22, genomic survey sequence.
ACCESSION BX153895
VERSION BX153895.1 GI:27985456
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 56)
AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 116L22. 116L22 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES Location/Qualifiers
source 1. .56
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-116L22"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
ORIGIN

Query Match 100.0%; Score 13; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 3.4e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAATAAACAGGG 13
||||||||||||
Db 28 AAAATAAACAGGG 40

RESULT 2
CF554321/c
LOCUS CF554321 92 bp mRNA linear EST 23-SEP-2003
DEFINITION SSHGgW69 Subtracted library from Infected wheat roots with

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 10.6399 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-5
Perfect score: 13
Sequence: 1 aaaataaacaggg 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13	100.0	13	13	ADT08246	Adt08246 Zebrafish
	2	13	100.0	13	13	ADT89054	Adt89054 Zebrafish
	3	13	100.0	217	4	AAK62657	Aak62657 Human imm
c	4	13	100.0	222	6	ADH32082	Adh32082 Yeast sma
	5	13	100.0	227	4	AAK83013	Aak83013 Human imm
	6	13	100.0	279	10	ADH83979	Adh83979 Enterococ
c	7	13	100.0	345	10	ADD32698	Add32698 Human mit
	8	13	100.0	349	4	AAK83015	Aak83015 Human imm
	9	13	100.0	349	4	AAK83014	Aak83014 Human imm
	10	13	100.0	353	4	AAL23714	Aal23714 Human bre
	11	13	100.0	415	13	ACN58810	Acn58810 Cotton gy
	12	13	100.0	435	13	ADT08242	Adt08242 Zebrafish
	13	13	100.0	435	13	ADT89050	Adt89050 Zebrafish
c	14	13	100.0	439	13	ACN58770	Acn58770 Cotton gy
c	15	13	100.0	458	12	ADL88319	Adl88319 DNA up-re
c	16	13	100.0	458	12	ADL88320	Adl88320 DNA up-re
	17	13	100.0	480	13	ADT08271	Adt08271 Zebrafish
	18	13	100.0	480	13	ADT89079	Adt89079 Zebrafish
c	19	13	100.0	493	5	ABV51847	Abv51847 Human pro
	20	13	100.0	500	9	ACH36331	Ach36331 Human end
	21	13	100.0	501	13	ACN61291	Acn61291 Cotton gy
c	22	13	100.0	508	5	ABA14249	Aba14249 Human ner
	23	13	100.0	512	12	ADP66310	Adp66310 Human cDN
c	24	13	100.0	522	4	ABA89508	Aba89508 Escherich
	25	13	100.0	563	5	ADI68794	Adi68794 Human ova
	26	13	100.0	563	5	ADI75153	Adi75153 Human ova
	27	13	100.0	566	5	ABV50018	Abv50018 Human pro
	28	13	100.0	593	12	ACH77328	Ach77328 Human gen
	29	13	100.0	603	13	ACN50391	Acn50391 Cotton no
c	30	13	100.0	649	13	ADR61743	Adr61743 Cotton cD
c	31	13	100.0	668	6	ABL89601	Abl89601 Human pol
c	32	13	100.0	720	13	ADT48592	Adt48592 Bacterial
	33	13	100.0	759	4	AAI94754	Aai94754 Human neu
c	34	13	100.0	807	2	AAZ42245	Aaz42245 Human nor
c	35	13	100.0	818	8	ABV77452	Abv77452 P. monodo
c	36	13	100.0	820	13	ADT18958	Adt18958 Plant cDN
	37	13	100.0	830	5	AAS63164	Aas63164 Human pur
	38	13	100.0	987	13	ADT45337	Adt45337 Bacterial
	39	13	100.0	1011	10	ACF68641	Acf68641 Photorhab
	40	13	100.0	1113	5	ADM19419	Adm19419 Novel hum
	41	13	100.0	1206	5	AAH94515	Aah94515 Human foe
c	42	13	100.0	1312	13	ADR60819	Adr60819 Cotton cD
	43	13	100.0	1529	6	ABS51334	Abs51334 cDNA enco
c	44	13	100.0	1693	2	AAV59721	Aav59721 Human sec
c	45	13	100.0	1693	6	ABS73711	Abs73711 Human cDN

ALIGNMENTS

RESULT 1
ADT08246
ID ADT08246 standard; DNA; 13 BP.
XX
AC ADT08246;
XX
DT 13-JAN-2005 (first entry)
XX
DE Zebrafish L-FABP upstream region HFH(2) binding site.
XX
KW Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer.
XX
OS Danio rerio.
XX
PN US2004209833-A1.
XX
PD 21-OCT-2004.
XX
PF 21-NOV-2003; 2003US-00717573.
XX
PR 16-APR-2003; 2003US-0463035P.
PR 27-MAY-2003; 2003US-0473210P.
XX
PA (WUJJ/) WU J.
PA (HERG/) HER G M.
XX
PI Wu J, Her GM;
XX
DR WPI; 2004-765481/75.
XX
PT New isolated polynucleotide useful for generating transgenic fish such as
PT zebrafish, comprises liver-specific expression control sequence that
PT modulates expression of vertebrate liver fatty acid binding protein.
XX
PS Claim 4; SEQ ID NO 5; 40pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a liver-
CC specific expression control sequence (LR) which modulates expression of a
CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 77.3396 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-5
Perfect score: 13
Sequence: 1 aaaataaacaggg 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	100.0	164	6	CQ659898	CQ659898 Sequence
c 2	13	100.0	204	6	AR553814	AR553814 Sequence
c 3	13	100.0	222	6	AX929191	AX929191 Sequence
4	13	100.0	263	10	BV289965	BV289965 S232P689F
5	13	100.0	273	10	AB135748	AB135748 Homo sapi
6	13	100.0	279	6	AR395849	AR395849 Sequence
7	13	100.0	299	6	AR522991	AR522991 Sequence
c 8	13	100.0	325	15	SCZ98154	Z98154 Secale cere
c 9	13	100.0	327	15	SCZ98153	Z98153 Secale cere
c 10	13	100.0	333	10	G10386	G10386 human STS C
11	13	100.0	353	6	CQ431150	CQ431150 Sequence
12	13	100.0	362	6	AR501629	AR501629 Sequence
13	13	100.0	362	6	AR516911	AR516911 Sequence
c 14	13	100.0	370	15	AF025512	AF025512 Citrus li
c 15	13	100.0	372	15	AY321660	AY321660 Citrus gr
c 16	13	100.0	372	15	AY321661	AY321661 Citrus au
c 17	13	100.0	372	15	AY321662	AY321662 Citrus ta
c 18	13	100.0	372	15	AY321663	AY321663 Citrus ju
c 19	13	100.0	372	15	AY321664	AY321664 Citrus er
c 20	13	100.0	372	15	AY321665	AY321665 Citrus su
c 21	13	100.0	372	15	AY321666	AY321666 Citrus be
c 22	13	100.0	372	15	AY321667	AY321667 Citrus ni
c 23	13	100.0	372	15	AY321668	AY321668 Citrus ta
c 24	13	100.0	372	15	AY321669	AY321669 Citrus ps
c 25	13	100.0	372	15	AY321670	AY321670 Citrus le
c 26	13	100.0	372	15	AY321671	AY321671 Citrus su
c 27	13	100.0	372	15	AY321673	AY321673 Citrus un
c 28	13	100.0	372	15	AY321674	AY321674 Citrus un
c 29	13	100.0	372	15	AY321675	AY321675 Citrus un
c 30	13	100.0	372	15	AY321676	AY321676 Citrus un
c 31	13	100.0	372	15	AY321677	AY321677 Citrus un
c 32	13	100.0	372	15	AY321678	AY321678 Citrus un
c 33	13	100.0	372	15	AY321679	AY321679 Fortunell
34	13	100.0	393	10	BV273156	BV273156 S235P682F
35	13	100.0	407	5	AB026035	AB026035 Gonostoma
36	13	100.0	411	10	AF191936	AF191936 Homo sapi
37	13	100.0	446	10	G41442	G41442 Z3334 Zebra
c 38	13	100.0	446	10	G41464	G41464 Z3782 Zebra
39	13	100.0	470	3	AY350324	AY350324 Unculture
40	13	100.0	472	10	BV215444	BV215444 S233P6221
41	13	100.0	477	10	BV677070	BV677070 ST10BE588
c 42	13	100.0	493	6	CQ519999	CQ519999 Sequence
43	13	100.0	503	6	BD118182	BD118182 EST and e
44	13	100.0	503	6	AR422629	AR422629 Sequence
45	13	100.0	503	6	AX983323	AX983323 Sequence

ALIGNMENTS

RESULT 1
CQ659898
LOCUS CQ659898 164 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 4824 from Patent WO02070737.
ACCESSION CQ659898
VERSION CQ659898.1 GI:42129537
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 4824 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES Location/Qualifiers
source 1. .164
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 13; DB 6; Length 164;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAATAAACAGGG 13
||||||||||||||
Db 52 AAAATAAACAGGG 64

RESULT 2
AR553814/c
LOCUS AR553814 204 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 8945 from patent US 6747137.
ACCESSION AR553814
VERSION AR553814.1 GI:53946989
KEYWORDS .
SOURCE Unknown.

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 11.548 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-5
Perfect score: 13
Sequence: 1 aaaataaacaggg 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		13	100.0	25	8	US-10-310-914A-70682	Sequence 70682, A
c 2		13	100.0	201	8	US-10-995-561-45580	Sequence 45580, A
c 3		13	100.0	201	8	US-10-995-561-45604	Sequence 45604, A
c 4		13	100.0	201	8	US-10-995-561-45606	Sequence 45606, A
c 5		13	100.0	201	8	US-10-995-561-45620	Sequence 45620, A
6		13	100.0	201	14	US-11-124-368A-7480	Sequence 7480, Ap
c 7		13	100.0	201	14	US-11-124-368A-17339	Sequence 17339, A
c 8		13	100.0	395	6	US-09-925-065A-182255	Sequence 182255,
9		13	100.0	397	10	US-10-301-480-298130	Sequence 298130,
10		13	100.0	397	10	US-10-301-480-298131	Sequence 298131,
11		13	100.0	397	10	US-10-301-480-911539	Sequence 911539,
12		13	100.0	397	10	US-10-301-480-911540	Sequence 911540,
13		13	100.0	413	6	US-09-925-065A-210863	Sequence 210863,
14		13	100.0	413	6	US-09-925-065A-210864	Sequence 210864,
c 15		13	100.0	417	6	US-09-925-065A-185779	Sequence 185779,
c 16		13	100.0	428	10	US-10-301-480-275960	Sequence 275960,
c 17		13	100.0	428	10	US-10-301-480-889369	Sequence 889369,
c 18		13	100.0	437	6	US-09-925-065A-856288	Sequence 856288,
c 19		13	100.0	447	6	US-09-925-065A-952784	Sequence 952784,
20		13	100.0	459	9	US-10-301-480-58009	Sequence 58009, A
21		13	100.0	459	9	US-10-301-480-58010	Sequence 58010, A
22		13	100.0	459	10	US-10-301-480-671418	Sequence 671418,
23		13	100.0	459	10	US-10-301-480-671419	Sequence 671419,
24		13	100.0	461	10	US-10-301-480-394300	Sequence 394300,
25		13	100.0	461	10	US-10-301-480-394301	Sequence 394301,
26		13	100.0	461	10	US-10-301-480-1007709	Sequence 1007709,
27		13	100.0	461	10	US-10-301-480-1007710	Sequence 1007710,
c 28		13	100.0	466	6	US-09-925-065A-473597	Sequence 473597,
29		13	100.0	467	6	US-09-925-065A-319550	Sequence 319550,
30		13	100.0	467	6	US-09-925-065A-319551	Sequence 319551,
31		13	100.0	480	10	US-10-301-480-554056	Sequence 554056,
32		13	100.0	480	10	US-10-301-480-1167465	Sequence 1167465,
33		13	100.0	497	6	US-09-925-065A-859863	Sequence 859863,
34		13	100.0	497	6	US-09-925-065A-859864	Sequence 859864,
c 35		13	100.0	510	10	US-10-301-480-479160	Sequence 479160,
c 36		13	100.0	510	10	US-10-301-480-1092569	Sequence 1092569,
c 37		13	100.0	511	6	US-09-925-065A-413114	Sequence 413114,
38		13	100.0	514	6	US-09-925-065A-315530	Sequence 315530,
39		13	100.0	514	6	US-09-925-065A-775950	Sequence 775950,
40		13	100.0	514	10	US-10-301-480-390539	Sequence 390539,
41		13	100.0	514	10	US-10-301-480-1003948	Sequence 1003948,
c 42		13	100.0	529	6	US-09-925-065A-501017	Sequence 501017,
c 43		13	100.0	531	6	US-09-925-065A-48752	Sequence 48752, A
c 44		13	100.0	531	9	US-10-301-480-149990	Sequence 149990,
c 45		13	100.0	531	10	US-10-301-480-763399	Sequence 763399,

ALIGNMENTS

RESULT 1
US-10-310-914A-70682
; Sequence 70682, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70682
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-70682

Query Match 100.0%; Score 13; DB 8; Length 25;
Best Local Similarity 92.3%; Pred. No. 5.2e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AAAATAAACAGGG 13
              ||||:|||||||
Db         10 AAAAUAAACAGGG 22
```

RESULT 2
US-10-995-561-45580/c
; Sequence 45580, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 15.1561 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-5
Perfect score: 13
Sequence: 1 aaaataaacaggg 13

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13	100.0	13	8	US-10-677-254-5	Sequence 5, Appli
	2	13	100.0	13	8	US-10-717-573-5	Sequence 5, Appli
c	3	13	100.0	25	7	US-10-719-956-112219	Sequence 112219,
c	4	13	100.0	25	8	US-10-719-900-439757	Sequence 439757,
	5	13	100.0	164	7	US-10-242-535A-4824	Sequence 4824, Ap
	6	13	100.0	164	7	US-10-085-783A-4824	Sequence 4824, Ap
c	7	13	100.0	201	7	US-10-741-601-23769	Sequence 23769, A
c	8	13	100.0	201	8	US-10-719-993-13530	Sequence 13530, A
c	9	13	100.0	201	8	US-10-741-600-57049	Sequence 57049, A
c	10	13	100.0	201	8	US-10-741-600-59352	Sequence 59352, A
c	11	13	100.0	201	8	US-10-741-600-59360	Sequence 59360, A
c	12	13	100.0	201	8	US-10-741-600-59362	Sequence 59362, A
c	13	13	100.0	201	8	US-10-741-600-64465	Sequence 64465, A
c	14	13	100.0	222	5	US-10-083-357-540	Sequence 540, App
	15	13	100.0	257	5	US-10-027-632-6566	Sequence 6566, Ap
	16	13	100.0	257	6	US-10-027-632-6566	Sequence 6566, Ap
c	17	13	100.0	258	7	US-10-424-599-131220	Sequence 131220,
	18	13	100.0	263	7	US-10-424-599-29916	Sequence 29916, A
c	19	13	100.0	271	8	US-10-425-115-6130	Sequence 6130, Ap
	20	13	100.0	273	8	US-10-674-124A-82	Sequence 82, Appl
	21	13	100.0	283	8	US-10-425-115-64382	Sequence 64382, A
c	22	13	100.0	335	8	US-10-425-115-105793	Sequence 105793,
	23	13	100.0	354	7	US-10-424-599-126370	Sequence 126370,
c	24	13	100.0	354	8	US-10-425-115-180952	Sequence 180952,
	25	13	100.0	361	7	US-10-437-963-32988	Sequence 32988, A
	26	13	100.0	364	8	US-10-425-115-17424	Sequence 17424, A
	27	13	100.0	366	7	US-10-424-599-24582	Sequence 24582, A
c	28	13	100.0	378	8	US-10-425-115-48051	Sequence 48051, A
	29	13	100.0	386	8	US-10-425-115-155338	Sequence 155338,
c	30	13	100.0	395	4	US-09-925-065A-182255	Sequence 182255,
c	31	13	100.0	412	7	US-10-424-599-92578	Sequence 92578, A
	32	13	100.0	413	4	US-09-925-065A-210863	Sequence 210863,
	33	13	100.0	413	4	US-09-925-065A-210864	Sequence 210864,
	34	13	100.0	415	7	US-10-021-323-13591	Sequence 13591, A
c	35	13	100.0	417	4	US-09-925-065A-185779	Sequence 185779,
c	36	13	100.0	421	7	US-10-424-599-22487	Sequence 22487, A
	37	13	100.0	421	7	US-10-424-599-132419	Sequence 132419,
c	38	13	100.0	425	8	US-10-425-115-174912	Sequence 174912,
	39	13	100.0	429	8	US-10-425-115-173184	Sequence 173184,
	40	13	100.0	435	8	US-10-677-254-1	Sequence 1, Appli
	41	13	100.0	435	8	US-10-717-573-1	Sequence 1, Appli
c	42	13	100.0	437	4	US-09-925-065A-856288	Sequence 856288,
c	43	13	100.0	439	7	US-10-021-323-13551	Sequence 13551, A
c	44	13	100.0	447	4	US-09-925-065A-952784	Sequence 952784,
c	45	13	100.0	449	5	US-10-027-632-42538	Sequence 42538, A

ALIGNMENTS

RESULT 1
US-10-677-254-5
; Sequence 5, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-5

Query Match 100.0%; Score 13; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AAAATAAACAGGG 13
              |||||||||||||
Db          1 AAAATAAACAGGG 13
```

RESULT 2
US-10-717-573-5
; Sequence 5, Application US/10717573
; Publication No. US20040209833A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/717,573
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 80.1483 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-4
Perfect score: 14
Sequence: 1 tccgataaacagaa 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	14	100.0	203	2	BF991217	BF991217 CM0-GN016
c	2	14	100.0	267	5	BW208810	BW208810 BW208810
	3	14	100.0	302	2	BE472387	BE472387 EST417240
c	4	14	100.0	360	1	AV203072	AV203072 AV203072
c	5	14	100.0	360	5	C42251	C42251 C42251 Yuji
	6	14	100.0	361	7	CO188886	CO188886 EK042317.
c	7	14	100.0	364	2	BE418639	BE418639 SCL072.G0
	8	14	100.0	376	7	CO177324	CO177324 EK053158.
	9	14	100.0	382	9	BZ667692	BZ667692 PUBIL22TD
c	10	14	100.0	386	9	AZ140106	AZ140106 SP_0004_A
	11	14	100.0	392	9	BH145141	BH145141 TDGET10TH
c	12	14	100.0	395	11	DE134893	DE134893 Oryzias l
	13	14	100.0	405	8	W38822	W38822 zb28a03.r1
c	14	14	100.0	411	5	C26016	C26016 C26016 Rice
c	15	14	100.0	430	9	CC888851	CC888851 SALK_1524
	16	14	100.0	430	11	DE047128	DE047128 Oryzias l
c	17	14	100.0	446	11	CR880560	CR880560 Sus scrof
	18	14	100.0	453	3	BJ514161	BJ514161 BJ514161
	19	14	100.0	454	3	BM173378	BM173378 900732 Av
	20	14	100.0	456	3	BM497296	BM497296 901150 Av
	21	14	100.0	462	1	AW906100	AW906100 EST342221
c	22	14	100.0	471	9	AQ047435	AQ047435 cLM-1a4-u
	23	14	100.0	477	9	CC788581	CC788581 ZMMBBb015
	24	14	100.0	480	7	CO275133	CO275133 EK116539.
c	25	14	100.0	486	7	CO833908	CO833908 LM_GH5_00
c	26	14	100.0	491	7	CO344064	CO344064 EP18616.3
	27	14	100.0	497	10	CW548561	CW548561 OA_ABa006
c	28	14	100.0	508	7	CO823729	CO823729 LM_GB5_00
c	29	14	100.0	510	9	AQ436576	AQ436576 HS_5051_B
	30	14	100.0	514	11	DE060732	DE060732 Oryzias l
	31	14	100.0	521	10	CW378170	CW378170 fsbb001f0
	32	14	100.0	523	10	CZ563626	CZ563626 1_p_bW038
	33	14	100.0	527	1	AW733371	AW733371 sk72f04.y
	34	14	100.0	533	11	DE135963	DE135963 Oryzias l
c	35	14	100.0	538	7	CO328538	CO328538 EK290834.
c	36	14	100.0	546	9	BZ349027	BZ349027 hp64g03.g
c	37	14	100.0	554	3	BI967882	BI967882 GM830003B
	38	14	100.0	561	8	CX699679	CX699679 86315.1 S
c	39	14	100.0	577	5	BU794121	BU794121 SJF2CCB10
c	40	14	100.0	579	10	BX139309	BX139309 Danio rer
c	41	14	100.0	581	5	BW291715	BW291715 BW291715
c	42	14	100.0	584	9	AZ921335	AZ921335 1006029D1
c	43	14	100.0	587	3	BJ520198	BJ520198 BJ520198
	44	14	100.0	589	11	DE053408	DE053408 Oryzias l
	45	14	100.0	595	3	BJ532783	BJ532783 BJ532783

ALIGNMENTS

RESULT 1
BF991217/c
LOCUS BF991217 203 bp mRNA linear EST 23-JAN-2001
DEFINITION CM0-GN0162-271000-627-h01 GN0162 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF991217
VERSION BF991217.1 GI:12397542
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 203)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM0&t2=CM0-GN0162-271000-627-h01&t3=2000-10-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 203.
FEATURES Location/Qualifiers
source 1. .203
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0162"

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 11.4583 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-4
Perfect score: 14
Sequence: 1 tccgataaacagaa 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14	100.0	14	13	ADT08245	Adt08245 Zebrafish
2	14	100.0	14	13	ADT89053	Adt89053 Zebrafish
3	14	100.0	435	13	ADT08242	Adt08242 Zebrafish
4	14	100.0	435	13	ADT89050	Adt89050 Zebrafish
5	14	100.0	480	13	ADT08271	Adt08271 Zebrafish
6	14	100.0	480	13	ADT89079	Adt89079 Zebrafish
7	14	100.0	966	8	ACA24900	Aca24900 Prokaryot
8	14	100.0	2033	13	ADT08244	Adt08244 Zebrafish
9	14	100.0	2033	13	ADT89052	Adt89052 Zebrafish
10	14	100.0	2783	13	ADT08243	Adt08243 Zebrafish
11	14	100.0	2783	13	ADT89051	Adt89051 Zebrafish
12	14	100.0	2960	13	ADT89080	Adt89080 Zebrafish
13	14	100.0	3795	13	ADR07856	Adr07856 Full leng
c 14	13	92.9	17	10	ADI49791	Adi49791 Human tum
15	13	92.9	426	6	ABZ31829	Abz31829 Candida a
c 16	13	92.9	441	10	ADK61530	Adk61530 Ovarian c
17	13	92.9	575	5	AAS72226	Aas72226 DNA encod
c 18	13	92.9	579	10	ADF03348	Adf03348 Bacterial
19	13	92.9	677	10	ACF67256	Acf67256 Photorhab
20	13	92.9	778	8	ACA48582	Aca48582 Prokaryot
c 21	13	92.9	813	3	AAF08645	Aaf08645 Fusarium
c 22	13	92.9	813	13	ADU52686	Adu52686 Fusarium
c 23	13	92.9	813	14	ADZ90689	Adz90689 Fusarium
c 24	13	92.9	822	13	ADT41711	Adt41711 Bacterial
25	13	92.9	957	8	ACA52235	Aca52235 Prokaryot
c 26	13	92.9	1062	8	ACA48942	Aca48942 Prokaryot
c 27	13	92.9	1065	8	ACA52246	Aca52246 Prokaryot
c 28	13	92.9	1077	11	ACH95736	Ach95736 Klebsiell
c 29	13	92.9	1104	6	ABK75373	Abk75373 Bacillus
c 30	13	92.9	1383	11	ACH98741	Ach98741 Klebsiell
c 31	13	92.9	1476	8	ABT19416	Abt19416 Aspergill
c 32	13	92.9	1605	8	ABT21236	Abt21236 Aspergill
c 33	13	92.9	1659	8	ABT18822	Abt18822 Aspergill
c 34	13	92.9	1659	8	ABT20638	Abt20638 Aspergill
35	13	92.9	1769	13	ADX46565	Adx46565 Plant ful
c 36	13	92.9	1861	6	ABK75009	Abk75009 Bacillus
37	13	92.9	2049	5	AAS90991	Aas90991 DNA encod
38	13	92.9	2687	4	ABL02107	Abl02107 Drosophil
39	13	92.9	3084	6	ABS65016	Abs65016 Invertebr
40	13	92.9	3455	2	AAV81385	Aav81385 Nucleic a
c 41	13	92.9	3659	8	ABT20042	Abt20042 Aspergill
c 42	13	92.9	3659	8	ABT18228	Abt18228 Aspergill
43	13	92.9	3703	4	ABL15078	Abl15078 Drosophil
c 44	13	92.9	3875	6	ABL61897	Abl61897 Colon ade
c 45	13	92.9	3875	6	ABN96818	Abn96818 Gene #331

ALIGNMENTS

RESULT 1
ADT08245
ID ADT08245 standard; DNA; 14 BP.
XX
AC ADT08245;
XX
DT 13-JAN-2005 (first entry)
XX
DE Zebrafish L-FABP upstream region HFH(1) binding site.
XX
KW Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer.
XX
OS Danio rerio.
XX
PN US2004209833-A1.
XX
PD 21-OCT-2004.
XX
PF 21-NOV-2003; 2003US-00717573.
XX
PR 16-APR-2003; 2003US-0463035P.
PR 27-MAY-2003; 2003US-0473210P.
XX
PA (WUJJ/) WU J.
PA (HERG/) HER G M.
XX
PI Wu J, Her GM;
XX
DR WPI; 2004-765481/75.
XX
PT New isolated polynucleotide useful for generating transgenic fish such as
PT zebrafish, comprises liver-specific expression control sequence that
PT modulates expression of vertebrate liver fatty acid binding protein.
XX
PS Claim 4; SEQ ID NO 4; 40pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a liver-
CC specific expression control sequence (LR) which modulates expression of a
CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 83.2888 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-4
Perfect score: 14
Sequence: 1 tccgataaacagaa 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		14	100.0	150	10	CR379981	CR379981 Arabidops
2		14	100.0	1007	6	AR503014	AR503014 Sequence
3		14	100.0	1007	6	AR518296	AR518296 Sequence
4	c	14	100.0	1045	13	AY494788	AY494788 Banana bu
5	c	14	100.0	2269	15	BT002394	BT002394 Arabidops
6		14	100.0	2960	5	AF512998	AF512998 Danio rer
7		14	100.0	3795	6	CQ850893	CQ850893 Sequence
8		14	100.0	3795	8	AK128090	AK128090 Homo sapi
9	c	14	100.0	15381	5	CR388056	CR388056 Zebrafish
10		14	100.0	21024	1	AE008736	AE008736 Salmonell
11		14	100.0	38000	2	CEF58A4	Z22179 Caenorhabdi
12	c	14	100.0	53155	5	BX511001	BX511001 Zebrafish
13	c	14	100.0	54620	14	AC014122	AC014122 Drosophil
14		14	100.0	58988	5	CR751229	CR751229 Zebrafish
15		14	100.0	71468	4	AC151393	AC151393 Atelerix
16	c	14	100.0	74832	8	AP000455	AP000455 Homo sapi
17	c	14	100.0	80867	5	BX908745	BX908745 Zebrafish
18	c	14	100.0	87501	5	BX001046	BX001046 Zebrafish
19	c	14	100.0	91897	5	CR394522	CR394522 Zebrafish
20	c	14	100.0	96656	5	BX950866	BX950866 Zebrafish
21	c	14	100.0	101678	14	CT009608	CT009608 Danio rer
22	c	14	100.0	104875	14	CT009605	CT009605 Danio rer
23	c	14	100.0	109342	5	BX465846	BX465846 Zebrafish
24	c	14	100.0	109430	14	CT009663	CT009663 Danio rer
25		14	100.0	110000	1	CR626927_30	Continuation (31 o
26		14	100.0	110000	1	CR626927_42	Continuation (43 o
27		14	100.0	110000	1	AE017220_09	Continuation (10 o
28		14	100.0	110000	1	AP006841_30	Continuation (31 o
29		14	100.0	110000	1	AP006841_43	Continuation (44 o
30		14	100.0	110000	1	BA000037_25	Continuation (26 o
31	c	14	100.0	110000	14	AC161108_1	Continuation (2 of
32		14	100.0	110000	15	CR382126_15	Continuation (16 o
33		14	100.0	110000	15	AP008209_360	Continuation (361
34		14	100.0	110000	15	AP008211_271	Continuation (272
35	c	14	100.0	111566	15	AC000348	AC000348 Genomic s
36		14	100.0	112314	5	BX897743	BX897743 Zebrafish
37	c	14	100.0	116542	5	AB075928	AB075928 Danio rer
38		14	100.0	116929	14	AL356001	AL356001 Homo sapi
39		14	100.0	118662	14	AC087569	AC087569 Arabidops
40	c	14	100.0	121253	5	CR352243	CR352243 Zebrafish
41	c	14	100.0	126083	5	CR339049	CR339049 Zebrafish
42		14	100.0	130669	8	AC108667	AC108667 Homo sapi
43	c	14	100.0	132833	5	BX255928	BX255928 Zebrafish
44	c	14	100.0	133128	5	BX276083	BX276083 Zebrafish
45	c	14	100.0	136155	5	CR407548	CR407548 Zebrafish

ALIGNMENTS

RESULT 1
CR379981
LOCUS CR379981 150 bp DNA linear STS 24-MAR-2004
DEFINITION Arabidopsis thaliana transposon insertion STS GT_5.29319, sequence tagged site.
ACCESSION CR379981
VERSION CR379981.1 GI:45726451
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B., Walsh,S., Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 150)
AUTHORS Clarke,J.H.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2004) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK
COMMENT AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3'end of the transposon, _5 denotes a sequence derived from the 5'end of the transposon BBSRC GARNet, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock code: N177848.
FEATURES Location/Qualifiers
source 1. .150
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="DSG7 X AC2"
/db_xref="taxon:3702"
/clone="AC000348"
/ecotype="Landsberg erecta NASC stock code NW20"
STS 1. .150
/standard_name="GT_5.29319"

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 2.79529 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-4
Perfect score: 14
Sequence: 1 tccgataaacagaa 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14	100.0	1007	3	US-09-270-767-7974	Sequence 7974, Ap
	2	14	100.0	1007	3	US-09-270-767-23256	Sequence 23256, A
c	3	14	100.0	236341	3	US-09-949-016-13978	Sequence 13978, A
	4	13	92.9	465	3	US-09-248-796A-937	Sequence 937, App
c	5	13	92.9	579	3	US-09-543-681A-3633	Sequence 3633, Ap
	6	13	92.9	789	3	US-09-248-796A-1577	Sequence 1577, Ap
c	7	13	92.9	813	3	US-09-533-559-1168	Sequence 1168, Ap
c	8	13	92.9	1077	3	US-09-489-039A-1531	Sequence 1531, Ap
c	9	13	92.9	1383	3	US-09-489-039A-4536	Sequence 4536, Ap
	10	13	92.9	3455	3	US-09-428-711A-20	Sequence 20, Appl
	11	13	92.9	10499	3	US-09-719-554-3	Sequence 3, Appli
	12	13	92.9	13537	3	US-09-949-016-17382	Sequence 17382, A
	13	13	92.9	61663	3	US-09-453-702B-62	Sequence 62, Appl
	14	13	92.9	61663	3	US-10-114-170-62	Sequence 62, Appl
c	15	12.6	90.0	601	3	US-09-949-002-1130	Sequence 1130, Ap
c	16	12.6	90.0	601	3	US-09-949-002-3943	Sequence 3943, Ap
c	17	12.6	90.0	601	3	US-09-949-002-5890	Sequence 5890, Ap
	18	12.4	88.6	25	3	US-09-396-196G-70899	Sequence 70899, A
	19	12.4	88.6	25	3	US-09-396-196G-70900	Sequence 70900, A
c	20	12.4	88.6	142	3	US-09-513-999C-15432	Sequence 15432, A
	21	12.4	88.6	189	3	US-09-513-999C-8950	Sequence 8950, Ap
	22	12.4	88.6	190	3	US-09-270-767-3065	Sequence 3065, Ap
	23	12.4	88.6	190	3	US-09-270-767-18347	Sequence 18347, A
c	24	12.4	88.6	200	3	US-09-513-999C-28659	Sequence 28659, A
	25	12.4	88.6	208	3	US-09-513-999C-33935	Sequence 33935, A
	26	12.4	88.6	231	3	US-09-248-796A-11587	Sequence 11587, A
c	27	12.4	88.6	276	3	US-09-313-294A-5656	Sequence 5656, Ap
c	28	12.4	88.6	336	3	US-09-248-796A-3061	Sequence 3061, Ap
	29	12.4	88.6	370	3	US-09-270-767-27452	Sequence 27452, A
c	30	12.4	88.6	390	3	US-09-107-532A-775	Sequence 775, App
	31	12.4	88.6	474	3	US-09-270-767-11810	Sequence 11810, A
	32	12.4	88.6	591	3	US-09-248-796A-8705	Sequence 8705, Ap
c	33	12.4	88.6	601	3	US-09-949-016-72991	Sequence 72991, A
c	34	12.4	88.6	601	3	US-09-949-016-72992	Sequence 72992, A
c	35	12.4	88.6	601	3	US-09-949-016-72993	Sequence 72993, A
c	36	12.4	88.6	601	3	US-09-949-016-72994	Sequence 72994, A
c	37	12.4	88.6	601	3	US-09-949-016-72995	Sequence 72995, A
c	38	12.4	88.6	601	3	US-09-949-016-84698	Sequence 84698, A
c	39	12.4	88.6	601	3	US-09-949-016-84699	Sequence 84699, A
	40	12.4	88.6	601	3	US-09-949-016-88177	Sequence 88177, A
c	41	12.4	88.6	601	3	US-09-949-016-154973	Sequence 154973,
c	42	12.4	88.6	601	3	US-09-949-016-154974	Sequence 154974,
	43	12.4	88.6	601	3	US-09-949-016-155353	Sequence 155353,
c	44	12.4	88.6	601	3	US-09-949-016-200667	Sequence 200667,
c	45	12.4	88.6	601	3	US-09-949-016-200813	Sequence 200813,

ALIGNMENTS

RESULT 1
US-09-270-767-7974
; Sequence 7974, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7974
; LENGTH: 1007
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7974

Query Match 100.0%; Score 14; DB 3; Length 1007;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGATAAACAGAA 14
||||||||||||||
Db 746 TCCGATAAACAGAA 759

RESULT 2
US-09-270-767-23256
; Sequence 23256, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23256
; LENGTH: 1007
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23256

Query Match 100.0%; Score 14; DB 3; Length 1007;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 12.4363 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-4
Perfect score: 14
Sequence: 1 tccgataaacagaa 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	14	100.0	483	6	US-09-925-065A-841694	Sequence 841694,
2	14	100.0	758	6	US-09-925-065A-32874	Sequence 32874, A
3	14	100.0	758	6	US-09-925-065A-32875	Sequence 32875, A
4	14	100.0	758	9	US-10-301-480-134112	Sequence 134112,
5	14	100.0	758	9	US-10-301-480-134113	Sequence 134113,
6	14	100.0	758	10	US-10-301-480-747521	Sequence 747521,
7	14	100.0	758	10	US-10-301-480-747522	Sequence 747522,
8	14	100.0	1725	11	US-11-096-568A-7427	Sequence 7427, Ap
9	13	92.9	22	8	US-10-310-914A-984498	Sequence 984498,
10	13	92.9	25	14	US-11-121-849-580786	Sequence 580786,
11	13	92.9	25	14	US-11-121-849-580787	Sequence 580787,
c 12	13	92.9	622	6	US-09-925-065A-844718	Sequence 844718,
c 13	13	92.9	622	6	US-09-925-065A-850883	Sequence 850883,
14	13	92.9	632	6	US-09-925-065A-851180	Sequence 851180,
15	13	92.9	1912	8	US-10-750-185-63544	Sequence 63544, A
16	13	92.9	1912	8	US-10-750-623-63544	Sequence 63544, A
c 17	13	92.9	214000	8	US-10-769-744-1	Sequence 1, Appli
c 18	13	92.9	214000	14	US-11-096-191-1	Sequence 1, Appli
c 19	12.6	90.0	558	6	US-09-925-065A-812079	Sequence 812079,
c 20	12.6	90.0	602	10	US-10-301-480-325251	Sequence 325251,
c 21	12.6	90.0	602	10	US-10-301-480-938660	Sequence 938660,
c 22	12.6	90.0	607	6	US-09-925-065A-244827	Sequence 244827,
23	12.4	88.6	18	8	US-10-310-914A-531359	Sequence 531359,
24	12.4	88.6	18	8	US-10-310-914A-1296266	Sequence 1296266,
25	12.4	88.6	19	12	US-11-101-244-124913	Sequence 124913,
26	12.4	88.6	19	12	US-11-101-244-1052921	Sequence 1052921,
27	12.4	88.6	19	13	US-11-083-784-124913	Sequence 124913,
28	12.4	88.6	19	13	US-11-083-784-1052921	Sequence 1052921,
c 29	12.4	88.6	24	8	US-10-310-914A-1059520	Sequence 1059520,
30	12.4	88.6	25	9	US-10-933-982-89901	Sequence 89901, A
31	12.4	88.6	50	11	US-11-146-428-174	Sequence 174, App
32	12.4	88.6	50	14	US-11-175-859-31258	Sequence 31258, A
33	12.4	88.6	50	14	US-11-175-859-91007	Sequence 91007, A
c 34	12.4	88.6	245	6	US-09-925-065A-38514	Sequence 38514, A
c 35	12.4	88.6	245	9	US-10-301-480-139752	Sequence 139752,
c 36	12.4	88.6	245	10	US-10-301-480-753161	Sequence 753161,
37	12.4	88.6	344	6	US-09-925-065A-258410	Sequence 258410,
c 38	12.4	88.6	406	14	US-11-000-688-353	Sequence 353, App
c 39	12.4	88.6	422	6	US-09-925-065A-292297	Sequence 292297,
c 40	12.4	88.6	430	10	US-10-301-480-369171	Sequence 369171,
c 41	12.4	88.6	430	10	US-10-301-480-982580	Sequence 982580,
42	12.4	88.6	436	10	US-10-301-480-297983	Sequence 297983,
43	12.4	88.6	436	10	US-10-301-480-911392	Sequence 911392,
44	12.4	88.6	437	6	US-09-925-065A-210690	Sequence 210690,
c 45	12.4	88.6	481	6	US-09-925-065A-956616	Sequence 956616,

ALIGNMENTS

RESULT 1
US-09-925-065A-841694
; Sequence 841694, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 841694
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-841694

Query Match 100.0%; Score 14; DB 6; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TCCGATAAACAGAA 14
              ||||||||||||||
Db        280 TCCGATAAACAGAA 293
```

RESULT 2
US-09-925-065A-32874
; Sequence 32874, Application US/09925065A

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 16.322 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-4
Perfect score: 14
Sequence: 1 tccgataaacagaa 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14	100.0	14	8	US-10-677-254-4	Sequence 4, Appli
	2	14	100.0	14	8	US-10-717-573-4	Sequence 4, Appli
	3	14	100.0	405	7	US-10-424-599-68519	Sequence 68519, A
c	4	14	100.0	412	7	US-10-424-599-20783	Sequence 20783, A
	5	14	100.0	435	8	US-10-677-254-1	Sequence 1, Appli
	6	14	100.0	435	8	US-10-717-573-1	Sequence 1, Appli
	7	14	100.0	480	8	US-10-677-254-30	Sequence 30, Appl
	8	14	100.0	480	8	US-10-717-573-30	Sequence 30, Appl
	9	14	100.0	483	4	US-09-925-065A-841694	Sequence 841694,
	10	14	100.0	758	4	US-09-925-065A-32874	Sequence 32874, A
	11	14	100.0	758	4	US-09-925-065A-32875	Sequence 32875, A
	12	14	100.0	775	7	US-10-424-599-64922	Sequence 64922, A
	13	14	100.0	966	7	US-10-282-122A-12770	Sequence 12770, A
	14	14	100.0	2033	8	US-10-677-254-3	Sequence 3, Appli
	15	14	100.0	2033	8	US-10-717-573-3	Sequence 3, Appli
	16	14	100.0	2783	8	US-10-677-254-2	Sequence 2, Appli
	17	14	100.0	2783	8	US-10-717-573-2	Sequence 2, Appli
c	18	13	92.9	25	7	US-10-719-956-424147	Sequence 424147,
c	19	13	92.9	25	9	US-10-956-157-53123	Sequence 53123, A
c	20	13	92.9	25	9	US-10-956-157-53124	Sequence 53124, A
c	21	13	92.9	25	9	US-10-956-157-53125	Sequence 53125, A
c	22	13	92.9	25	9	US-10-956-157-53126	Sequence 53126, A
c	23	13	92.9	25	9	US-10-956-157-137248	Sequence 137248,
c	24	13	92.9	25	9	US-10-843-527-90367	Sequence 90367, A
	25	13	92.9	25	9	US-10-843-527-146346	Sequence 146346,
	26	13	92.9	201	8	US-10-719-993-9873	Sequence 9873, Ap
c	27	13	92.9	201	8	US-10-719-993-32438	Sequence 32438, A
c	28	13	92.9	201	8	US-10-719-993-32440	Sequence 32440, A
	29	13	92.9	201	8	US-10-719-993-32504	Sequence 32504, A
	30	13	92.9	201	8	US-10-719-993-32514	Sequence 32514, A
	31	13	92.9	365	7	US-10-437-963-42369	Sequence 42369, A
	32	13	92.9	404	6	US-10-062-674-579	Sequence 579, App
	33	13	92.9	426	6	US-10-032-585-6116	Sequence 6116, Ap
c	34	13	92.9	441	9	US-10-505-680-700	Sequence 700, App
c	35	13	92.9	467	7	US-10-424-599-36463	Sequence 36463, A
c	36	13	92.9	530	7	US-10-424-599-17599	Sequence 17599, A
	37	13	92.9	575	9	US-10-450-763-8030	Sequence 8030, Ap
c	38	13	92.9	600	9	US-10-972-079-71408	Sequence 71408, A
c	39	13	92.9	600	9	US-10-972-079-71409	Sequence 71409, A
c	40	13	92.9	622	4	US-09-925-065A-844718	Sequence 844718,
c	41	13	92.9	622	4	US-09-925-065A-850883	Sequence 850883,
	42	13	92.9	632	4	US-09-925-065A-851180	Sequence 851180,
	43	13	92.9	778	7	US-10-282-122A-36452	Sequence 36452, A
c	44	13	92.9	813	8	US-10-653-047-1168	Sequence 1168, Ap
c	45	13	92.9	822	6	US-10-369-493-40149	Sequence 40149, A

ALIGNMENTS

RESULT 1
US-10-677-254-4
; Sequence 4, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDIN
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-4

Query Match 100.0%; Score 14; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TCCGATAAACAGAA 14
              ||||||||||||||
Db          1 TCCGATAAACAGAA 14
```

RESULT 2
US-10-717-573-4
; Sequence 4, Application US/10717573
; Publication No. US20040209833A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDIN
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/717,573
; CURRENT FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 14
; TYPE: DNA

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 1805.93 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-3
Perfect score: 2033
Sequence: 1 gtttttaatagtttttatgc.....gttgagcttctccagaaagc 2033

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	92	4.5	119036	8	US-10-995-561-13314	Sequence 13314, A
	2	91.6	4.5	396	11	US-11-250-759-53	Sequence 53, Appl
c	3	84	4.1	305312	8	US-10-995-561-13236	Sequence 13236, A
	4	83.8	4.1	5501	8	US-10-240-708-38	Sequence 38, Appl
	5	83.8	4.1	49979	8	US-10-995-561-13443	Sequence 13443, A
	6	82.8	4.1	8961	8	US-10-240-708-80	Sequence 80, Appl
	7	82.6	4.1	674	10	US-10-301-480-532538	Sequence 532538,
	8	82.6	4.1	674	10	US-10-301-480-1145947	Sequence 1145947,
	9	81.8	4.0	5562	8	US-10-240-708-63	Sequence 63, Appl
	10	81.4	4.0	105550	8	US-10-995-561-13235	Sequence 13235, A
	11	81.2	4.0	6070	8	US-10-240-708-10	Sequence 10, Appl
	12	81	4.0	5152	8	US-10-240-708-47	Sequence 47, Appl
	13	80.8	4.0	5844	8	US-10-240-708-89	Sequence 89, Appl
	14	80.6	4.0	7001	14	US-11-011-332A-103	Sequence 103, App
	15	80.4	4.0	28536	14	US-11-011-332A-155	Sequence 155, App
c	16	80.4	4.0	687411	9	US-10-330-773-26	Sequence 26, Appl
c	17	80.2	3.9	171486	14	US-11-121-086-105	Sequence 105, App
c	18	80.2	3.9	173602	14	US-11-121-086-25	Sequence 25, Appl
	19	79.6	3.9	6499	14	US-11-011-332A-91	Sequence 91, Appl
	20	79.6	3.9	173602	14	US-11-121-086-25	Sequence 25, Appl
	21	79.2	3.9	26772	8	US-10-995-561-13313	Sequence 13313, A
	22	79.2	3.9	54946	8	US-10-995-561-13479	Sequence 13479, A
c	23	79	3.9	1230	6	US-09-925-065A-77682	Sequence 77682, A
c	24	79	3.9	1230	6	US-09-925-065A-77683	Sequence 77683, A
c	25	79	3.9	1230	6	US-09-925-065A-77684	Sequence 77684, A
c	26	79	3.9	1230	9	US-10-301-480-178921	Sequence 178921,
c	27	79	3.9	1230	9	US-10-301-480-178922	Sequence 178922,
c	28	79	3.9	1230	9	US-10-301-480-178923	Sequence 178923,
c	29	79	3.9	1230	10	US-10-301-480-792330	Sequence 792330,
c	30	79	3.9	1230	10	US-10-301-480-792331	Sequence 792331,
c	31	79	3.9	1230	10	US-10-301-480-792332	Sequence 792332,
c	32	78.8	3.9	1230	6	US-09-925-065A-77681	Sequence 77681, A
c	33	78.8	3.9	1230	9	US-10-301-480-178920	Sequence 178920,
c	34	78.8	3.9	1230	10	US-10-301-480-792329	Sequence 792329,
	35	78.8	3.9	8607	8	US-10-240-708-72	Sequence 72, Appl
	36	78.8	3.9	28536	14	US-11-011-332A-151	Sequence 151, App
	37	78	3.8	6499	14	US-11-011-332A-77	Sequence 77, Appl
	38	77.8	3.8	9001	14	US-11-011-332A-4	Sequence 4, Appli
	39	77.6	3.8	991	10	US-10-301-480-568792	Sequence 568792,
	40	77.6	3.8	991	10	US-10-301-480-568795	Sequence 568795,
	41	77.6	3.8	991	10	US-10-301-480-1182201	Sequence 1182201,
	42	77.6	3.8	991	10	US-10-301-480-1182204	Sequence 1182204,
	43	77	3.8	6306	8	US-10-240-708-50	Sequence 50, Appl
	44	76.4	3.8	679	6	US-09-925-065A-685065	Sequence 685065,
	45	76.4	3.8	3641	14	US-11-102-026A-181	Sequence 181, App

ALIGNMENTS

RESULT 1
US-10-995-561-13314/c
; Sequence 13314, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13314
; LENGTH: 119036
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(119036)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13314

Query Match 4.5%; Score 92; DB 8; Length 119036;
Best Local Similarity 50.0%; Pred. No. 0.042;
Matches 256; Conservative 0; Mismatches 255; Indels 1; Gaps 1;

```
Qy      1066 TTTATTAAAGATTATTTTATTTATTTATTATTTTATTTATCTATTTATTTATTTAGTTGT 1125
             | | ||| | ||| || ||| ||||| ||| |     ||||  || | ||| || ||
Db     31721 TATTTTATATATTTTTATATATATTTTATATATATAAAATCTTATTTTATATATATTTTA 31662

Qy      1126 TTATTTATTCCTGCAGATCATGCCTTGTGCCTTTTTACATTTAATTTAATTTTTAATTTA 1185
             | |  ||  | | || |   | | |   | | || ||  ||| | |||||  || ||
Db     31661 TATATATTTTATATATATAAAATCATAT-TTTATATATATAAAATCTTATTTTATATATA 31603

Qy      1186 ATTTCCTTTTATTTTTTTTTATTTTTTATTTTATTTATTTTACAGTCTGACAAATACT 1245
              |||   | | || | | | |  | ||  |||   | ||||||     | | | ||||  |
Db     31602 TTTTATATATTTTATATATAAAATCTTATTTTATATATATTTTTATATATAAAAAATCAT 31543

Qy      1246 GAACTAAAAACCTCTCAGATCATGTCTATGCATTTCATTTTATTTTATTTCATTTTATAT 1305
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 2370.19 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-3
Perfect score: 2033
Sequence: 1 gtttttaatagtttttatgc.....gttgagcttctccagaaagc 2033

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2033	100.0	2033	8	US-10-677-254-3	Sequence 3, Appli
	2	2033	100.0	2033	8	US-10-717-573-3	Sequence 3, Appli
	3	2033	100.0	2783	8	US-10-677-254-2	Sequence 2, Appli
	4	2033	100.0	2783	8	US-10-717-573-2	Sequence 2, Appli
	5	863	42.4	1086	8	US-10-677-254-27	Sequence 27, Appl
	6	863	42.4	1086	8	US-10-717-573-27	Sequence 27, Appl
	7	480	23.6	480	8	US-10-677-254-30	Sequence 30, Appl
	8	480	23.6	480	8	US-10-717-573-30	Sequence 30, Appl
	9	435	21.4	435	8	US-10-677-254-1	Sequence 1, Appli
	10	435	21.4	435	8	US-10-717-573-1	Sequence 1, Appli
	11	220.2	10.8	13382	8	US-10-612-594-4	Sequence 4, Appli
c	12	198.6	9.8	3003	9	US-10-511-362-9	Sequence 9, Appli
c	13	193.2	9.5	5563	5	US-10-136-734-26	Sequence 26, Appl
c	14	185.6	9.1	7495	7	US-10-742-828-5	Sequence 5, Appli
c	15	185.6	9.1	7508	7	US-10-742-828-4	Sequence 4, Appli
c	16	184.8	9.1	13382	8	US-10-612-594-4	Sequence 4, Appli
	17	126.4	6.2	1062	8	US-10-425-115-120013	Sequence 120013,
	18	123.6	6.1	3673778	6	US-10-312-841-2	Sequence 2, Appli
	19	121.4	6.0	14006	6	US-10-311-455-1931	Sequence 1931, Ap
c	20	119.6	5.9	510510	8	US-10-741-600-17606	Sequence 17606, A
c	21	119.2	5.9	2520	7	US-10-389-566-205	Sequence 205, App
c	22	118.4	5.8	1214	7	US-10-424-599-102083	Sequence 102083,
	23	117.8	5.8	446	3	US-09-960-352-3400	Sequence 3400, Ap
	24	117.8	5.8	6109	6	US-10-311-455-299	Sequence 299, App
	25	117.8	5.8	6109	7	US-10-221-613-33	Sequence 33, Appl
	26	117.4	5.8	17934	6	US-10-311-455-1692	Sequence 1692, Ap
	27	117.2	5.8	6419	6	US-10-311-455-240	Sequence 240, App
c	28	117.2	5.8	71843	9	US-10-488-292-3	Sequence 3, Appli
	29	116.4	5.7	12237	6	US-10-311-455-2331	Sequence 2331, Ap
	30	116.2	5.7	6668	6	US-10-311-455-1670	Sequence 1670, Ap
	31	115.8	5.7	921	8	US-10-425-115-38710	Sequence 38710, A
	32	115.8	5.7	1204	7	US-10-437-963-77858	Sequence 77858, A
	33	115.8	5.7	16033	6	US-10-311-455-1377	Sequence 1377, Ap
	34	115.4	5.7	1039	8	US-10-425-115-58802	Sequence 58802, A
	35	115.2	5.7	803	7	US-10-437-963-72176	Sequence 72176, A
	36	114.2	5.6	996	8	US-10-425-115-151933	Sequence 151933,
	37	114	5.6	6286	7	US-10-221-714A-313	Sequence 313, App
	38	113.8	5.6	6145	6	US-10-311-455-945	Sequence 945, App
	39	113.8	5.6	7597	6	US-10-311-455-986	Sequence 986, App
c	40	113.6	5.6	739	8	US-10-425-115-55020	Sequence 55020, A
	41	113.6	5.6	1243	8	US-10-425-115-172717	Sequence 172717,
c	42	113.6	5.6	1300	7	US-10-668-749A-1	Sequence 1, Appli
	43	113.2	5.6	1121	8	US-10-425-115-115706	Sequence 115706,
	44	112.6	5.5	1004	8	US-10-425-115-81106	Sequence 81106, A
	45	112.4	5.5	3683	8	US-10-473-126-339	Sequence 339, App

ALIGNMENTS

RESULT 1
US-10-677-254-3
; Sequence 3, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2033
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-3

Query Match 100.0%; Score 2033; DB 8; Length 2033;
Best Local Similarity 100.0%; Pred. No. 1.6e-308;
Matches 2033; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTTTTTAATAGTTTTTATGCCATTTTAAGGTCAATATTATTAGCCCCTTTAAGCTATTTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTTTTAATAGTTTTTATGCCATTTTAAGGTCAATATTATTAGCCCCTTTAAGCTATTTT 60

Qy         61 TTTTCGATAGTCTACAGAACAAACCATCGGTATACAATGACTTGCCTAATTACCCTAACC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTTCGATAGTCTACAGAACAAACCATCGGTATACAATGACTTGCCTAATTACCCTAACC 120

Qy        121 TGCCTAGTTACCCTAATTAACCTAGTTAAGCCTTTAAATGTCACTTTAAGCTGTATAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCCTAGTTACCCTAATTAACCTAGTTAAGCCTTTAAATGTCACTTTAAGCTGTATAGAA 180

Qy        181 GTGTCTTGAAGAATATCTAGTCTAATATTATTGACTGTCATCATGGCAAAGATAAAATAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGTCTTGAAGAATATCTAGTCTAATATTATTGACTGTCATCATGGCAAAGATAAAATAA 240

Qy        241 ATCAGTTATTAAAACTATTATGATTAGAAATGTGCTGAAACAATCTGCTCTCCGATAAAC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATCAGTTATTAAAACTATTATGATTAGAAATGTGCTGAAACAATCTGCTCTCCGATAAAC 300

Qy        301 AGAAATTGAACAAAATAAACAGGGGGGCTAATAAATTTAAGGGGTTAAATAATTCTGATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 405.917 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-3
Perfect score: 2033
Sequence: 1 gtttttaatagtttttatgc.....gttgagcttctccagaaagc 2033

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	122	6.0	612	3	US-09-902-540-1357	Sequence 1357, Ap
c	2	109	5.4	1039	3	US-09-902-540-1280	Sequence 1280, Ap
c	3	104	5.1	614	3	US-09-902-540-1318	Sequence 1318, Ap
c	4	97.8	4.8	187169	3	US-09-949-016-12776	Sequence 12776, A
c	5	97.8	4.8	191569	3	US-09-949-016-15940	Sequence 15940, A
	6	97.6	4.8	451924	3	US-09-949-016-12896	Sequence 12896, A
	7	97.6	4.8	451925	3	US-09-949-016-17305	Sequence 17305, A
	8	94.8	4.7	147382	3	US-09-949-016-14624	Sequence 14624, A
	9	94.6	4.7	658	3	US-08-998-416-595	Sequence 595, App
	10	91.6	4.5	396	3	US-09-640-173-53	Sequence 53, Appl
	11	91.6	4.5	396	3	US-09-713-550-53	Sequence 53, Appl
	12	91.6	4.5	396	3	US-09-825-294-53	Sequence 53, Appl
	13	91.6	4.5	396	3	US-09-970-966-53	Sequence 53, Appl
c	14	90.8	4.5	19124	2	US-08-487-826B-13	Sequence 13, Appl
	15	88.6	4.4	134987	3	US-09-949-016-15348	Sequence 15348, A
	16	88.6	4.4	134987	3	US-09-949-016-15349	Sequence 15349, A
	17	88.6	4.4	134987	3	US-09-949-016-15350	Sequence 15350, A
	18	88.6	4.4	134987	3	US-09-949-016-15507	Sequence 15507, A
	19	88.6	4.4	134987	3	US-09-949-016-15508	Sequence 15508, A
	20	88.6	4.4	134987	3	US-09-949-016-15509	Sequence 15509, A
c	21	88.4	4.3	4167	3	US-09-973-278-700	Sequence 700, App
	22	86.6	4.3	29717	3	US-09-949-016-16284	Sequence 16284, A
	23	86.6	4.3	60376	3	US-09-949-016-12423	Sequence 12423, A
c	24	84.2	4.1	1132	3	US-09-533-559-5452	Sequence 5452, Ap
	25	84	4.1	57507	3	US-09-949-016-15019	Sequence 15019, A
	26	83.8	4.1	19438	3	US-09-949-016-12699	Sequence 12699, A
c	27	83.4	4.1	55886	3	US-09-949-016-15129	Sequence 15129, A
c	28	83.2	4.1	6243	2	US-09-056-075-1	Sequence 1, Appli
	29	81.8	4.0	601	3	US-09-949-016-196365	Sequence 196365,
	30	81.8	4.0	601	3	US-09-949-016-196366	Sequence 196366,
	31	80.6	4.0	55264	3	US-09-949-016-15014	Sequence 15014, A
	32	80.6	4.0	94755	3	US-09-949-016-11839	Sequence 11839, A
	33	80	3.9	50000	3	US-09-662-254B-25	Sequence 25, Appl
c	34	79.4	3.9	240	2	US-08-628-417-6	Sequence 6, Appli
	35	79.2	3.9	601	3	US-09-949-016-196367	Sequence 196367,
	36	79.2	3.9	25590	3	US-09-949-002-777	Sequence 777, App
	37	78.6	3.9	7218	2	US-08-232-463-14	Sequence 14, Appl
c	38	78.6	3.9	32392	3	US-09-662-254B-27	Sequence 27, Appl
c	39	78.4	3.9	119153	3	US-09-949-016-12378	Sequence 12378, A
c	40	78.2	3.8	2447	2	US-09-014-969-14	Sequence 14, Appl
	41	77.8	3.8	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	42	77.8	3.8	133719	3	US-09-949-016-15092	Sequence 15092, A
c	43	77.4	3.8	3680	3	US-09-647-390-15	Sequence 15, Appl
c	44	76.8	3.8	1696	3	US-09-835-811-1	Sequence 1, Appli
c	45	76	3.7	41736	3	US-09-949-016-17091	Sequence 17091, A

ALIGNMENTS

RESULT 1
US-09-902-540-1357/c
; Sequence 1357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1357
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

Query Match 6.0%; Score 122; DB 3; Length 612;
Best Local Similarity 55.4%; Pred. No. 1.6e-12;
Matches 255; Conservative 0; Mismatches 202; Indels 3; Gaps 1;

```
Qy       1060 TTTAAGTTTATTAAAGATTATTTTATTTATTTATTATTTTATTTATCTATTTATTTATTT 1119
              |||   ||| ||        |||| ||| ||| || |||| ||| | | ||| ||| |||
Db        572 TTTTTTTTTTTTTTTTTAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 513

Qy       1120 AGTTGTTTATTTATTCCTGCAGATCATGCCTTGTGCCTTTTTACATTTAATTTAATTTTT 1179
                || ||| ||| ||  |      |  |   || |   |||||   |||   ||| |||||
Db        512 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTATTATTTTTT 453

Qy       1180 AATTTAATTTCCTTTTATTTTTTTTTATTTTTTTATTTTATTTTATTTTACAGTCTGACA 1239
              |||||  |||   ||| ||||||||| ||||||| ||||||||| ||||    |
Db        452 AATTTTTTTTTAATTTTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTATTTT 393

Qy       1240 AATACTGAACTAAAAACCTCTCAGATCATGTCTATGCATTTCATTTTATTTTATTTCA-- 1297
              ||| |  ||        | | |  |  | | |||  ||||  ||||  ||| |||
Db        392 TATATTTTATTTTTTTTTTTTATTTTTTTTTTATTTATTTTTTTTTTATTTTTTTANTT 333

Qy       1298 -TTTTATATTATTAATTTTAATATTTTTATTTTACAGTCTGACAAATACTGAATTAAAAA 1356
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 11638.7 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-3
Perfect score: 2033
Sequence: 1 gtttttaatagtttttatgc.....gttgagcttctccagaaagc 2033

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	250.4	12.3	762	10	BX218760	BX218760 Danio rer
c 2	247.4	12.2	738	10	BX240588	BX240588 Danio rer
c 3	247.4	12.2	823	10	BX208028	BX208028 Danio rer
c 4	247.4	12.2	838	10	BX132903	BX132903 Danio rer
c 5	245.2	12.1	677	8	DN901058	DN901058 naq14d10.
6	244.8	12.0	525	3	BM572872	BM572872 fx50g08.y
7	244.8	12.0	822	10	BX161705	BX161705 Danio rer
c 8	242.6	11.9	712	10	BX189345	BX189345 Danio rer
9	242.6	11.9	777	10	BX153299	BX153299 Danio rer
c 10	241.8	11.9	712	10	BX188692	BX188692 Danio rer
11	241.6	11.9	745	10	BX183629	BX183629 Danio rer
c 12	237.6	11.7	743	10	BX198263	BX198263 Danio rer
c 13	236	11.6	741	10	BX139380	BX139380 Danio rer
14	235	11.6	849	8	DN858051	DN858051 naa21e09.
15	234.6	11.5	452	7	CK676851	CK676851 ZF101-P00
16	234.4	11.5	421	1	AW419795	AW419795 fj83e07.y
17	234	11.5	662	10	BX193504	BX193504 Danio rer
c 18	233.6	11.5	629	10	BX218791	BX218791 Danio rer
c 19	233.6	11.5	691	10	BX195342	BX195342 Danio rer
20	232.8	11.5	554	1	AI588386	AI588386 fc01b09.x
21	232.8	11.5	623	1	AL720634	AL720634 AL720634
c 22	232.6	11.4	715	10	BX213266	BX213266 Danio rer
23	232.6	11.4	829	10	BX157343	BX157343 Danio rer
c 24	232.4	11.4	741	10	BX231206	BX231206 Danio rer
25	232.2	11.4	477	10	BX165718	BX165718 Danio rer
c 26	231.6	11.4	803	10	BX241500	BX241500 Danio rer
27	231.4	11.4	752	10	BX244449	BX244449 Danio rer
28	231.2	11.4	647	10	BX199272	BX199272 Danio rer
29	230.8	11.4	744	10	BX176747	BX176747 Danio rer
c 30	230.4	11.3	659	10	BX163107	BX163107 Danio rer
c 31	230	11.3	833	10	BX227411	BX227411 Danio rer
c 32	229.6	11.3	778	10	BX147912	BX147912 Danio rer
c 33	229	11.3	765	10	BX133288	BX133288 Danio rer
34	228.8	11.3	685	10	BX206202	BX206202 Danio rer
35	228.6	11.2	542	10	BX133575	BX133575 Danio rer
c 36	228.6	11.2	986	6	CA477668	CA477668 AGENCOURT
c 37	228.4	11.2	612	11	DR17L4S	AL733963 Danio rer
c 38	228.4	11.2	802	1	AL719686	AL719686 AL719686
c 39	228.2	11.2	735	10	BX172233	BX172233 Danio rer
40	228.2	11.2	830	6	CD758553	CD758553 AGENCOURT
41	228	11.2	500	6	CD581432	CD581432 RK012A4H1
c 42	227.6	11.2	612	11	DR7B5S	AL746477 Danio rer
43	227.6	11.2	615	10	BX137736	BX137736 Danio rer
44	227.6	11.2	723	10	BX225086	BX225086 Danio rer
45	227	11.2	709	10	BX224896	BX224896 Danio rer

ALIGNMENTS

RESULT 1
BX218760/c
LOCUS BX218760 762 bp DNA linear GSS 13-MAR-2003
DEFINITION Danio rerio genomic clone DKEY-47D4, genomic survey sequence.
ACCESSION BX218760
VERSION BX218760.1 GI:28050646
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 762)
AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 47D4. 47D4 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES Location/Qualifiers
source 1. .762
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-47D4"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
ORIGIN

Query Match 12.3%; Score 250.4; DB 10; Length 762;
Best Local Similarity 84.6%; Pred. No. 3e-30;
Matches 325; Conservative 0; Mismatches 36; Indels 23; Gaps 3;

```
Qy          3 TTTTAATAGTTTTTATGCCATTTTAAGGTCAATATTATTAGCCCCTTTAAGCTATTTTTT 62
              |||| |   ||| |  ||||||||||||||| |||||||||||||||| |||| ||||
Db        590 TTTTTAATTTTTAAAAACCATTTTAAGGTCAAAATTATTAGCCCCTTTAACCTATATTTT 531

Qy         63 TTCGATAGTCTACAGAACAAACCATCGGTATACAATGACTTGCCTAATTACCCTAACCTG 122
              |||||| |||||||||||||||||  |||||||| ||||||||||||||||||||||||
Db        530 TTCGATCGTCTACAGAACAAACCATCATTATACAATAACTTGCCTAATTACCCTAACCTG 471

Qy        123 CCTAGTTACCCTAATTAACCTAGTTAAGCCTTTAAATGTCACTTTAAGCTGTATAGAAGT 182
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 1663.92 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-3
Perfect score: 2033
Sequence: 1 gtttttaatagtttttatgc.....gttgagcttctccagaaagc 2033

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2033	100.0	2033	13	ADT08244	Adt08244 Zebrafish
	2	2033	100.0	2033	13	ADT89052	Adt89052 Zebrafish
	3	2033	100.0	2783	13	ADT08243	Adt08243 Zebrafish
	4	2033	100.0	2783	13	ADT89051	Adt89051 Zebrafish
	5	2033	100.0	2960	13	ADT89080	Adt89080 Zebrafish
	6	863	42.4	1086	13	ADT08268	Adt08268 Zebrafish
	7	863	42.4	1086	13	ADT89076	Adt89076 Zebrafish
	8	480	23.6	480	13	ADT08271	Adt08271 Zebrafish
	9	480	23.6	480	13	ADT89079	Adt89079 Zebrafish
	10	435	21.4	435	13	ADT08242	Adt08242 Zebrafish
	11	435	21.4	435	13	ADT89050	Adt89050 Zebrafish
	12	232.4	11.4	78064	13	ADS17402	Ads17402 Nucleotid
c	13	224.8	11.1	78064	13	ADS17402	Ads17402 Nucleotid
	14	220.2	10.8	13382	14	ADW44488	Adw44488 Zebrafish
c	15	198.6	9.8	3003	10	ADF18692	Adf18692 Zebrafish
c	16	193.2	9.5	5563	2	AAX08941	Aax08941 GATA-1 pr
c	17	185.6	9.1	7495	13	ADR30815	Adr30815 Zebrafish
c	18	185.6	9.1	7508	13	ADR30814	Adr30814 Zebrafish
c	19	184.8	9.1	13382	14	ADW44488	Adw44488 Zebrafish
c	20	122	6.0	612	14	ACL64894	Acl64894 M. xanthu
	21	121.4	6.0	14006	6	ABL33958	Abl33958 Human imm
c	22	119.2	5.9	2520	12	ADJ48201	Adj48201 Maize oil
	23	117.8	5.8	446	8	ABX38235	Abx38235 Bovine ES
	24	117.8	5.8	6109	6	ABL32326	Abl32326 Human imm
	25	117.8	5.8	6109	6	AAS61077	Aas61077 Human gen
	26	117.6	5.8	700	10	ACD92384	Acd92384 Human col
c	27	117.6	5.8	6644	2	AAX33181	Aax33181 Base sequ
c	28	117.6	5.8	7372	2	AAX33182	Aax33182 Base sequ
c	29	117.6	5.8	7797	2	AAX33180	Aax33180 Cowpox vi
c	30	117.6	5.8	7996	2	AAX33184	Aax33184 Base sequ
	31	117.4	5.8	17934	6	ABL33719	Abl33719 Human imm
	32	117.2	5.8	6419	6	ABL32267	Abl32267 Human imm
c	33	117.2	5.8	71843	8	ACC79619	Acc79619 Zebrafish
	34	116.4	5.7	12237	6	ABL34358	Abl34358 Human imm
	35	116.2	5.7	6668	6	ABL33697	Abl33697 Human imm
	36	115.8	5.7	16033	6	ABL33404	Abl33404 Human imm
	37	114	5.6	6286	4	AAS46591	Aas46591 Tumour su
	38	113.8	5.6	6145	6	ABL32972	Abl32972 Human imm
	39	113.8	5.6	7597	6	ABL33013	Abl33013 Human imm
c	40	113.6	5.6	1000	12	ADQ62833	Adq62833 Homopoly-
	41	113.6	5.6	1000	12	ADQ62832	Adq62832 Homopoly-
c	42	113.6	5.6	1300	12	ADP85917	Adp85917 Synthetic
	43	112.4	5.5	3683	8	ABZ10199	Abz10199 Haematopo
c	44	112	5.5	556	6	ABQ36997	Abq36997 Oligonucl
	45	112	5.5	556	6	ABQ36996	Abq36996 Oligonucl

ALIGNMENTS

RESULT 1
ADT08244
ID ADT08244 standard; DNA; 2033 BP.
XX
AC ADT08244;
XX
DT 13-JAN-2005 (first entry)
XX
DE Zebrafish L-FABP upstream region -2033 to -1.
XX
KW Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer.
XX
OS Danio rerio.
XX
PN US2004209833-A1.
XX
PD 21-OCT-2004.
XX
PF 21-NOV-2003; 2003US-00717573.
XX
PR 16-APR-2003; 2003US-0463035P.
PR 27-MAY-2003; 2003US-0473210P.
XX
PA (WUJJ/) WU J.
PA (HERG/) HER G M.
XX
PI Wu J, Her GM;
XX
DR WPI; 2004-765481/75.
XX
PT New isolated polynucleotide useful for generating transgenic fish such as
PT zebrafish, comprises liver-specific expression control sequence that
PT modulates expression of vertebrate liver fatty acid binding protein.
XX
PS Claim 11; SEQ ID NO 3; 40pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a liver-
CC specific expression control sequence (LR) which modulates expression of a
CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

comprising base pairs

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 12094.7 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-3
Perfect score: 2033
Sequence: 1 gtttttaatagtttttatgc.....gttgagcttctccagaaagc 2033

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2033	100.0	2960	5	AF512998	AF512998 Danio rer
c	2	1164.6	57.3	178271	5	CR293507	CR293507 Zebrafish
	3	306.6	15.1	80017	5	AL845372	AL845372 Zebrafish
c	4	295.4	14.5	150673	14	CR361557	CR361557 Danio rer
	5	295	14.5	85762	5	CR388368	CR388368 Zebrafish
c	6	274.4	13.5	223535	14	CR376787	CR376787 Danio rer
	7	273	13.4	192644	14	CR762383	CR762383 Danio rer
c	8	272.6	13.4	173481	5	AL928671	AL928671 Zebrafish
c	9	268.6	13.2	110000	14	CR753903_0	CR753903 Danio rer
c	10	268.4	13.2	222975	14	CR848050	CR848050 Danio rer
c	11	265.6	13.1	169046	5	AL928828	AL928828 Zebrafish
c	12	265.2	13.0	170625	14	CR854833	CR854833 Danio rer
	13	264.8	13.0	109430	14	CT009663	CT009663 Danio rer
	14	264.8	13.0	149742	5	CR382286	CR382286 Zebrafish
c	15	264.8	13.0	169758	5	CR936240	CR936240 Zebrafish
	16	264.4	13.0	117304	5	BX470100	BX470100 Zebrafish
c	17	264.4	13.0	202883	14	BX470165	BX470165 Danio rer
c	18	263.8	13.0	143812	5	BX957262	BX957262 Zebrafish
	19	263.8	13.0	172321	5	AL844171	AL844171 Zebrafish
	20	263.2	12.9	304914	14	BX942830	BX942830 Danio rer
c	21	262.8	12.9	165603	5	BX548250	BX548250 Zebrafish
c	22	261	12.8	171841	14	AL928708	AL928708 Danio rer
	23	260.2	12.8	179240	5	BX005309	BX005309 Zebrafish
c	24	259.8	12.8	156150	5	BX322540	BX322540 Zebrafish
c	25	259.8	12.8	167345	5	BX004771	BX004771 Zebrafish
	26	259	12.7	190968	5	BX465217	BX465217 Zebrafish
	27	258.8	12.7	185806	14	CR933100	CR933100 Danio rer
	28	258.6	12.7	152840	5	AL732567	AL732567 Zebrafish
	29	258.4	12.7	200760	5	AL928872	AL928872 Zebrafish
	30	258.2	12.7	182255	14	CR938723	CR938723 Danio rer
c	31	257.8	12.7	185855	5	CR759734	CR759734 Zebrafish
c	32	257.8	12.7	191769	14	CR933561	CR933561 Danio rer
c	33	257.8	12.7	192592	5	AL929096	AL929096 Zebrafish
	34	257.4	12.7	136156	14	CR847502	CR847502 Danio rer
c	35	257.4	12.7	148815	14	CR376750	CR376750 Danio rer
c	36	257.2	12.7	185384	14	CR391914	CR391914 Danio rer
	37	257.2	12.7	203371	14	AC139623	AC139623 Danio rer
	38	257	12.6	151770	14	CR925754	CR925754 Danio rer
c	39	257	12.6	289569	14	CR382321	CR382321 Danio rer
	40	256.8	12.6	105764	5	CR385077	CR385077 Zebrafish
	41	256.8	12.6	153159	14	CR936337	CR936337 Danio rer
	42	256.6	12.6	162436	5	AL929535	AL929535 Zebrafish
c	43	256	12.6	149630	14	CR628386	CR628386 Danio rer
c	44	256	12.6	165139	14	CR925756	CR925756 Danio rer
	45	256	12.6	201151	14	BX511097	BX511097 Danio rer

ALIGNMENTS

RESULT 1
AF512998
LOCUS AF512998 2960 bp DNA linear VRT 10-JUL-2003
DEFINITION Danio rerio liver-type fatty acid binding protein gene, partial cds.
ACCESSION AF512998
VERSION AF512998.1 GI:21314558
KEYWORDS .
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 2960)
AUTHORS Her,G.M., Yeh,Y.H. and Wu,J.L.
TITLE 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish
JOURNAL Dev. Dyn. 227 (3), 347-356 (2003)
PUBMED 12815620
REFERENCE 2 (bases 1 to 2960)
AUTHORS Her,G.M. and Wu,J.-L.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chiu-Yuan Road, Sec. 2, Taipei 115, Taiwan
FEATURES Location/Qualifiers
source 1. .2960
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
mRNA <2784. .>2960
/product="liver-type fatty acid binding protein"
CDS 2784. .>2960
/note="Lfabp; small cytosolic protein involved in lipid transport and metabolism"
/codon_start=1
/product="liver-type fatty acid binding protein"
/protein_id="AAM47005.1"
/db_xref="GI:21314559"
/translation="MAFSGTWQVYAQENYEEFLRAISLPEEVIKLAKDVKPVTEIQQN GSDFTITSKTPGKTV"

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 555.664 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-2
Perfect score: 2783
Sequence: 1 gcagtaaattgattcaaact.....gttgagcttctccagaaagc 2783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

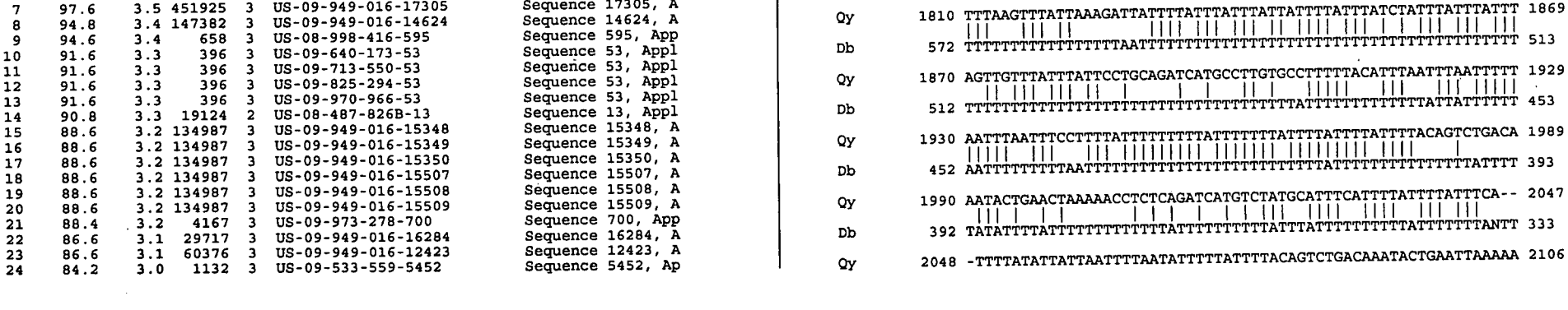
SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	122	4.4	612	3	US-09-902-540-1357	Sequence 1357, Ap
c	2	109	3.9	1039	3	US-09-902-540-1280	Sequence 1280, Ap
c	3	104	3.7	614	3	US-09-902-540-1318	Sequence 1318, Ap
c	4	97.8	3.5	187169	3	US-09-949-016-12776	Sequence 12776, A
c	5	97.8	3.5	191569	3	US-09-949-016-15940	Sequence 15940, A
	6	97.6	3.5	451924	3	US-09-949-016-12896	Sequence 12896, A
	7	97.6	3.5	451925	3	US-09-949-016-17305	Sequence 17305, A
	8	94.8	3.4	147382	3	US-09-949-016-14624	Sequence 14624, A
	9	94.6	3.4	658	3	US-08-998-416-595	Sequence 595, App
	10	91.6	3.3	396	3	US-09-640-173-53	Sequence 53, Appl
	11	91.6	3.3	396	3	US-09-713-550-53	Sequence 53, Appl
	12	91.6	3.3	396	3	US-09-825-294-53	Sequence 53, Appl
	13	91.6	3.3	396	3	US-09-970-966-53	Sequence 53, Appl
c	14	90.8	3.3	19124	2	US-08-487-826B-13	Sequence 13, Appl
	15	88.6	3.2	134987	3	US-09-949-016-15348	Sequence 15348, A
	16	88.6	3.2	134987	3	US-09-949-016-15349	Sequence 15349, A
	17	88.6	3.2	134987	3	US-09-949-016-15350	Sequence 15350, A
	18	88.6	3.2	134987	3	US-09-949-016-15507	Sequence 15507, A
	19	88.6	3.2	134987	3	US-09-949-016-15508	Sequence 15508, A
	20	88.6	3.2	134987	3	US-09-949-016-15509	Sequence 15509, A
c	21	88.4	3.2	4167	3	US-09-973-278-700	Sequence 700, App
	22	86.6	3.1	29717	3	US-09-949-016-16284	Sequence 16284, A
	23	86.6	3.1	60376	3	US-09-949-016-12423	Sequence 12423, A
c	24	84.2	3.0	1132	3	US-09-533-559-5452	Sequence 5452, Ap
	25	84	3.0	57507	3	US-09-949-016-15019	Sequence 15019, A
	26	83.8	3.0	19438	3	US-09-949-016-12699	Sequence 12699, A
c	27	83.4	3.0	55886	3	US-09-949-016-15129	Sequence 15129, A
c	28	83.2	3.0	6243	2	US-09-056-075-1	Sequence 1, Appli
	29	81.8	2.9	601	3	US-09-949-016-196365	Sequence 196365,
	30	81.8	2.9	601	3	US-09-949-016-196366	Sequence 196366,
	31	80.6	2.9	55264	3	US-09-949-016-15014	Sequence 15014, A
	32	80.6	2.9	94755	3	US-09-949-016-11839	Sequence 11839, A
	33	80	2.9	50000	3	US-09-662-254B-25	Sequence 25, Appl
c	34	79.4	2.9	240	2	US-08-628-417-6	Sequence 6, Appli
	35	79.2	2.8	601	3	US-09-949-016-196367	Sequence 196367,
	36	79.2	2.8	25590	3	US-09-949-002-777	Sequence 777, App
	37	78.6	2.8	7218	2	US-08-232-463-14	Sequence 14, Appl
c	38	78.6	2.8	32392	3	US-09-662-254B-27	Sequence 27, Appl
c	39	78.4	2.8	119153	3	US-09-949-016-12378	Sequence 12378, A
c	40	78.2	2.8	2447	2	US-09-014-969-14	Sequence 14, Appl
	41	77.8	2.8	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	42	77.8	2.8	133719	3	US-09-949-016-15092	Sequence 15092, A
c	43	77.4	2.8	3680	3	US-09-647-390-15	Sequence 15, Appl
c	44	76.8	2.8	1696	3	US-09-835-811-1	Sequence 1, Appli
c	45	76.6	2.8	1141	3	US-09-806-708B-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-902-540-1357/c
; Sequence 1357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1357
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

Query Match 4.4%; Score 122; DB 3; Length 612;
Best Local Similarity 55.4%; Pred. No. 9.3e-14;
Matches 255; Conservative 0; Mismatches 202; Indels 3; Gaps 1;



GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 2277.76 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-2
Perfect score: 2783
Sequence: 1 gcagtaaattgattcaaact.....gttgagcttctccagaaagc 2783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2783	100.0	2783	13	ADT08243	Adt08243 Zebrafish
	2	2783	100.0	2783	13	ADT89051	Adt89051 Zebrafish
	3	2783	100.0	2960	13	ADT89080	Adt89080 Zebrafish
	4	2033	73.1	2033	13	ADT08244	Adt08244 Zebrafish
	5	2033	73.1	2033	13	ADT89052	Adt89052 Zebrafish
	6	863	31.0	1086	13	ADT08268	Adt08268 Zebrafish
	7	863	31.0	1086	13	ADT89076	Adt89076 Zebrafish
	8	480	17.2	480	13	ADT08271	Adt08271 Zebrafish
	9	480	17.2	480	13	ADT89079	Adt89079 Zebrafish
	10	435	15.6	435	13	ADT08242	Adt08242 Zebrafish
	11	435	15.6	435	13	ADT89050	Adt89050 Zebrafish
	12	348	12.5	71843	8	ACC79619	Acc79619 Zebrafish
	13	260.4	9.4	78064	13	ADS17402	Ads17402 Nucleotid
c	14	257.6	9.3	78064	13	ADS17402	Ads17402 Nucleotid
	15	251.4	9.0	13382	14	ADW44488	Adw44488 Zebrafish
c	16	217.6	7.8	13382	14	ADW44488	Adw44488 Zebrafish
c	17	207.2	7.4	3003	10	ADF18692	Adf18692 Zebrafish
c	18	206.8	7.4	7495	13	ADR30815	Adr30815 Zebrafish
c	19	206.8	7.4	7508	13	ADR30814	Adr30814 Zebrafish
c	20	200.8	7.2	5563	2	AAX08941	Aax08941 GATA-1 pr
c	21	122	4.4	612	14	ACL64894	Acl64894 M. xanthu
	22	121.4	4.4	14006	6	ABL33958	Abl33958 Human imm
c	23	119.2	4.3	2520	12	ADJ48201	Adj48201 Maize oil
	24	117.8	4.2	446	8	ABX38235	Abx38235 Bovine ES
	25	117.8	4.2	6109	6	ABL32326	Abl32326 Human imm
	26	117.8	4.2	6109	6	AAS61077	Aas61077 Human gen
	27	117.6	4.2	700	10	ACD92384	Acd92384 Human col
c	28	117.6	4.2	6644	2	AAX33181	Aax33181 Base sequ
c	29	117.6	4.2	7372	2	AAX33182	Aax33182 Base sequ
c	30	117.6	4.2	7797	2	AAX33180	Aax33180 Cowpox vi
c	31	117.6	4.2	7996	2	AAX33184	Aax33184 Base sequ
	32	117.4	4.2	17934	6	ABL33719	Abl33719 Human imm
	33	117.2	4.2	6419	6	ABL32267	Abl32267 Human imm
c	34	117.2	4.2	71843	8	ACC79619	Acc79619 Zebrafish
	35	116.4	4.2	12237	6	ABL34358	Abl34358 Human imm
	36	116.2	4.2	6668	6	ABL33697	Abl33697 Human imm
	37	115.8	4.2	16033	6	ABL33404	Abl33404 Human imm
	38	114	4.1	6286	4	AAS46591	Aas46591 Tumour su
	39	113.8	4.1	6145	6	ABL32972	Abl32972 Human imm
	40	113.8	4.1	7597	6	ABL33013	Abl33013 Human imm
c	41	113.6	4.1	1000	12	ADQ62833	Adq62833 Homopoly-
	42	113.6	4.1	1000	12	ADQ62832	Adq62832 Homopoly-
c	43	113.6	4.1	1300	12	ADP85917	Adp85917 Synthetic
c	44	112.6	4.0	8056	8	ABZ10246	Abz10246 Haematopo
	45	112.4	4.0	3683	8	ABZ10199	Abz10199 Haematopo

ALIGNMENTS

RESULT 1
ADT08243
ID ADT08243 standard; DNA; 2783 BP.
XX
AC ADT08243;
XX
DT 13-JAN-2005 (first entry)
XX
DE Zebrafish L-FABP upstream region plus some coding region.
XX
KW Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer; promoter.
XX
OS Danio rerio.
XX
PN US2004209833-A1.
XX
PD 21-OCT-2004.
XX
PF 21-NOV-2003; 2003US-00717573.
XX
PR 16-APR-2003; 2003US-0463035P.
PR 27-MAY-2003; 2003US-0473210P.
XX
PA (WUJJ/) WU J.
PA (HERG/) HER G M.
XX
PI Wu J, Her GM;
XX
DR WPI; 2004-765481/75.
XX
PT New isolated polynucleotide useful for generating transgenic fish such as
PT zebrafish, comprises liver-specific expression control sequence that
PT modulates expression of vertebrate liver fatty acid binding protein.
XX
PS Claim 10; SEQ ID NO 2; 40pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a liver-
CC specific expression control sequence (LR) which modulates expression of a
CC vertebrate liver fatty acid binding protein (L-FABP). Also included are a

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 16556.6 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-2
Perfect score: 2783
Sequence: 1 gcagtaaattgattcaaact.....gttgagcttctccagaaagc 2783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2783	100.0	2960	5	AF512998	AF512998 Danio rer
c 2	1828	65.7	178271	5	CR293507	CR293507 Zebrafish
c 3	521.8	18.7	132182	14	CR848746	CR848746 Danio rer
4	520	18.7	168638	14	CR548631	CR548631 Danio rer
c 5	518	18.6	159232	5	BX119923	BX119923 Zebrafish
6	515.8	18.5	195837	14	AL953868	AL953868 Danio rer
7	512.6	18.4	160252	5	CR847928	CR847928 Zebrafish
c 8	512.4	18.4	168638	14	CR548631	CR548631 Danio rer
9	512.4	18.4	178075	14	CR847790	CR847790 Danio rer
10	512.4	18.4	182255	14	CR938723	CR938723 Danio rer
11	510.4	18.3	73696	5	AL772143	AL772143 Zebrafish
c 12	510.4	18.3	85075	14	BX681415	BX681415 Danio rer
c 13	510.4	18.3	162045	5	CR318660	CR318660 Zebrafish
c 14	510.2	18.3	216472	5	CR356243	CR356243 Zebrafish
15	508	18.3	112811	5	BX005301	BX005301 Zebrafish
16	508	18.3	169760	5	BX511310	BX511310 Zebrafish
c 17	507.8	18.2	201525	5	AL954172	AL954172 Zebrafish
18	507.2	18.2	187161	5	BX088526	BX088526 Zebrafish
c 19	506.4	18.2	74150	14	BX927093	BX927093 Danio rer
20	506.4	18.2	152488	14	CR407597	CR407597 Danio rer
c 21	505.4	18.2	145294	5	CR354539	CR354539 Zebrafish
c 22	505.4	18.2	178457	5	AL935031	AL935031 Zebrafish
c 23	504.4	18.1	202138	5	BX004991	BX004991 Zebrafish
c 24	504	18.1	149598	5	BX957346	BX957346 Zebrafish
25	504	18.1	157294	14	CR848023	CR848023 Danio rer
c 26	503.4	18.1	178425	5	CR354429	CR354429 Zebrafish
c 27	502.6	18.1	169310	5	BX323461	BX323461 Zebrafish
c 28	502.4	18.1	146348	5	CR548627	CR548627 Zebrafish
29	502.2	18.0	217527	14	CR394525	CR394525 Danio rer
c 30	501.4	18.0	176982	5	AL732610	AL732610 Zebrafish
31	501.4	18.0	232594	5	BX005006	BX005006 Zebrafish
c 32	501.2	18.0	107132	5	BX255941	BX255941 Zebrafish
33	500.8	18.0	158133	5	BX000348	BX000348 Zebrafish
c 34	499.2	17.9	178247	5	BX248504	BX248504 Zebrafish
35	498	17.9	155693	14	CR524823	CR524823 Danio rer
36	497.2	17.9	149008	14	BX296524	BX296524 Danio rer
c 37	497.2	17.9	149329	14	BX511217	BX511217 Danio rer
c 38	497	17.9	110000	14	AL954295_2	Continuation (3 of
39	497	17.9	110000	14	AL954295_5	Continuation (6 of
40	497	17.9	130060	5	AL929217	AL929217 Zebrafish
41	497	17.9	141118	14	CR391998	CR391998 Danio rer
c 42	495.8	17.8	127576	5	AC144824	AC144824 Danio rer
43	495.2	17.8	137166	5	AL929566	AL929566 Zebrafish
44	495.2	17.8	166869	14	BX005359	BX005359 Danio rer
45	495	17.8	205568	5	BX470184	BX470184 Zebrafish

ALIGNMENTS

RESULT 1
AF512998
LOCUS AF512998 2960 bp DNA linear VRT 10-JUL-2003
DEFINITION Danio rerio liver-type fatty acid binding protein gene, partial cds.
ACCESSION AF512998
VERSION AF512998.1 GI:21314558
KEYWORDS .
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 2960)
AUTHORS Her,G.M., Yeh,Y.H. and Wu,J.L.
TITLE 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish
JOURNAL Dev. Dyn. 227 (3), 347-356 (2003)
PUBMED 12815620
REFERENCE 2 (bases 1 to 2960)
AUTHORS Her,G.M. and Wu,J.-L.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chiu-Yuan Road, Sec. 2, Taipei 115, Taiwan
FEATURES Location/Qualifiers
source 1. .2960
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
mRNA <2784. .>2960
/product="liver-type fatty acid binding protein"
CDS 2784. .>2960
/note="Lfabp; small cytosolic protein involved in lipid transport and metabolism"
/codon_start=1
/product="liver-type fatty acid binding protein"
/protein_id="AAM47005.1"
/db_xref="GI:21314559"
/translation="MAFSGTWQVYAQENYEEFLRAISLPEEVIKLAKDVKPVTEIQQN GSDFTITSKTPGKTV"

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 2472.16 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-2
Perfect score: 2783
Sequence: 1 gcagtaaattgattcaaact.....gttgagcttctccagaaagc 2783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	92	3.3	119036	8	US-10-995-561-13314	Sequence 13314, A
	2	91.6	3.3	396	11	US-11-250-759-53	Sequence 53, Appl
c	3	84	3.0	305312	8	US-10-995-561-13236	Sequence 13236, A
	4	83.8	3.0	5501	8	US-10-240-708-38	Sequence 38, Appl
	5	83.8	3.0	49979	8	US-10-995-561-13443	Sequence 13443, A
	6	82.8	3.0	8961	8	US-10-240-708-80	Sequence 80, Appl
	7	82.6	3.0	674	10	US-10-301-480-532538	Sequence 532538,
	8	82.6	3.0	674	10	US-10-301-480-1145947	Sequence 1145947,
	9	81.8	2.9	5562	8	US-10-240-708-63	Sequence 63, Appl
	10	81.4	2.9	105550	8	US-10-995-561-13235	Sequence 13235, A
	11	81.2	2.9	6070	8	US-10-240-708-10	Sequence 10, Appl
	12	81	2.9	5152	8	US-10-240-708-47	Sequence 47, Appl
	13	80.8	2.9	5844	8	US-10-240-708-89	Sequence 89, Appl
	14	80.6	2.9	7001	14	US-11-011-332A-103	Sequence 103, App
	15	80.4	2.9	28536	14	US-11-011-332A-155	Sequence 155, App
c	16	80.4	2.9	687411	9	US-10-330-773-26	Sequence 26, Appl
c	17	80.2	2.9	171486	14	US-11-121-086-105	Sequence 105, App
c	18	80.2	2.9	173602	14	US-11-121-086-25	Sequence 25, Appl
	19	79.6	2.9	6499	14	US-11-011-332A-91	Sequence 91, Appl
	20	79.6	2.9	173602	14	US-11-121-086-25	Sequence 25, Appl
	21	79.2	2.8	26772	8	US-10-995-561-13313	Sequence 13313, A
	22	79.2	2.8	54946	8	US-10-995-561-13479	Sequence 13479, A
c	23	79	2.8	1230	6	US-09-925-065A-77682	Sequence 77682, A
c	24	79	2.8	1230	6	US-09-925-065A-77683	Sequence 77683, A
c	25	79	2.8	1230	6	US-09-925-065A-77684	Sequence 77684, A
c	26	79	2.8	1230	9	US-10-301-480-178921	Sequence 178921,
c	27	79	2.8	1230	9	US-10-301-480-178922	Sequence 178922,
c	28	79	2.8	1230	9	US-10-301-480-178923	Sequence 178923,
c	29	79	2.8	1230	10	US-10-301-480-792330	Sequence 792330,
c	30	79	2.8	1230	10	US-10-301-480-792331	Sequence 792331,
c	31	79	2.8	1230	10	US-10-301-480-792332	Sequence 792332,
c	32	78.8	2.8	1230	6	US-09-925-065A-77681	Sequence 77681, A
c	33	78.8	2.8	1230	9	US-10-301-480-178920	Sequence 178920,
c	34	78.8	2.8	1230	10	US-10-301-480-792329	Sequence 792329,
	35	78.8	2.8	8607	8	US-10-240-708-72	Sequence 72, Appl
	36	78.8	2.8	28536	14	US-11-011-332A-151	Sequence 151, App
	37	78	2.8	6499	14	US-11-011-332A-77	Sequence 77, Appl
	38	77.8	2.8	9001	14	US-11-011-332A-4	Sequence 4, Appli
	39	77.6	2.8	991	10	US-10-301-480-568792	Sequence 568792,
	40	77.6	2.8	991	10	US-10-301-480-568795	Sequence 568795,
	41	77.6	2.8	991	10	US-10-301-480-1182201	Sequence 1182201,
	42	77.6	2.8	991	10	US-10-301-480-1182204	Sequence 1182204,
	43	77	2.8	6306	8	US-10-240-708-50	Sequence 50, Appl
	44	76.4	2.7	679	6	US-09-925-065A-685065	Sequence 685065,
	45	76.4	2.7	3641	14	US-11-102-026A-181	Sequence 181, App

ALIGNMENTS

RESULT 1
US-10-995-561-13314/c
; Sequence 13314, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13314
; LENGTH: 119036
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(119036)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13314

Query Match 3.3%; Score 92; DB 8; Length 119036;
Best Local Similarity 50.0%; Pred. No. 0.027;
Matches 256; Conservative 0; Mismatches 255; Indels 1; Gaps 1;

```
Qy       1816 TTTATTAAAGATTATTTTATTTATTTATTATTTTATTTATCTATTTATTTATTTAGTTGT 1875
             | | ||| | ||| || ||| |||||  ||| |     ||||  || | ||| || ||
Db      31721 TATTTTATATATTTTTATATATATTTTATATATATAAAATCTTATTTTATATATATTTTA 31662

Qy       1876 TTATTTATTCCTGCAGATCATGCCTTGTGCCTTTTTACATTTAATTTAATTTTTAATTTA 1935
             | |  ||  | | || |   | | |   | | || ||  ||| | |||||  || ||
Db      31661 TATATATTTTATATATATAAAATCATAT-TTTATATATATAAAATCTTATTTTATATATA 31603

Qy       1936 ATTTCCTTTTATTTTTTTTTATTTTTTTATTTTATTTTATTTTACAGTCTGACAAATACT 1995
               |||   | | || | | | |  | ||  |||   | ||||||    | | | ||||  |
Db      31602 TTTTATATATTTTATATATAAAATCTTATTTTATATATATTTTTATATATAAAAAATCAT 31543

Qy       1996 GAACTAAAAACCTCTCAGATCATGTCTATGCATTTCATTTTATTTTATTTCATTTTATAT 2055
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 3244.58 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-2
Perfect score: 2783
Sequence: 1 gcagtaaattgattcaaact.....gttgagcttctccagaaagc 2783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2783	100.0	2783	8	US-10-677-254-2	Sequence 2, Appli
	2	2783	100.0	2783	8	US-10-717-573-2	Sequence 2, Appli
	3	2033	73.1	2033	8	US-10-677-254-3	Sequence 3, Appli
	4	2033	73.1	2033	8	US-10-717-573-3	Sequence 3, Appli
	5	863	31.0	1086	8	US-10-677-254-27	Sequence 27, Appl
	6	863	31.0	1086	8	US-10-717-573-27	Sequence 27, Appl
	7	480	17.2	480	8	US-10-677-254-30	Sequence 30, Appl
	8	480	17.2	480	8	US-10-717-573-30	Sequence 30, Appl
	9	435	15.6	435	8	US-10-677-254-1	Sequence 1, Appli
	10	435	15.6	435	8	US-10-717-573-1	Sequence 1, Appli
	11	348	12.5	71843	9	US-10-488-292-3	Sequence 3, Appli
c	12	318.6	11.4	602	7	US-10-663-561-333	Sequence 333, App
	13	251.4	9.0	13382	8	US-10-612-594-4	Sequence 4, Appli
c	14	217.6	7.8	13382	8	US-10-612-594-4	Sequence 4, Appli
c	15	207.2	7.4	3003	9	US-10-511-362-9	Sequence 9, Appli
c	16	206.8	7.4	7495	7	US-10-742-828-5	Sequence 5, Appli
c	17	206.8	7.4	7508	7	US-10-742-828-4	Sequence 4, Appli
c	18	200.8	7.2	5563	5	US-10-136-734-26	Sequence 26, Appl
	19	126.4	4.5	1062	8	US-10-425-115-120013	Sequence 120013,
	20	123.6	4.4	3673778	6	US-10-312-841-2	Sequence 2, Appli
	21	121.4	4.4	14006	6	US-10-311-455-1931	Sequence 1931, Ap
c	22	119.6	4.3	510510	8	US-10-741-600-17606	Sequence 17606, A
c	23	119.2	4.3	2520	7	US-10-389-566-205	Sequence 205, App
c	24	118.4	4.3	1214	7	US-10-424-599-102083	Sequence 102083,
	25	117.8	4.2	446	3	US-09-960-352-3400	Sequence 3400, Ap
	26	117.8	4.2	6109	6	US-10-311-455-299	Sequence 299, App
	27	117.8	4.2	6109	7	US-10-221-613-33	Sequence 33, Appl
	28	117.4	4.2	17934	6	US-10-311-455-1692	Sequence 1692, Ap
	29	117.2	4.2	6419	6	US-10-311-455-240	Sequence 240, App
c	30	117.2	4.2	71843	9	US-10-488-292-3	Sequence 3, Appli
	31	116.4	4.2	12237	6	US-10-311-455-2331	Sequence 2331, Ap
	32	116.2	4.2	6668	6	US-10-311-455-1670	Sequence 1670, Ap
	33	115.8	4.2	921	8	US-10-425-115-38710	Sequence 38710, A
	34	115.8	4.2	1204	7	US-10-437-963-77858	Sequence 77858, A
	35	115.8	4.2	16033	6	US-10-311-455-1377	Sequence 1377, Ap
	36	115.4	4.1	1039	8	US-10-425-115-58802	Sequence 58802, A
	37	115.2	4.1	803	7	US-10-437-963-72176	Sequence 72176, A
	38	114.2	4.1	996	8	US-10-425-115-151933	Sequence 151933,
	39	114	4.1	6286	7	US-10-221-714A-313	Sequence 313, App
	40	113.8	4.1	6145	6	US-10-311-455-945	Sequence 945, App
	41	113.8	4.1	7597	6	US-10-311-455-986	Sequence 986, App
c	42	113.6	4.1	739	8	US-10-425-115-55020	Sequence 55020, A
	43	113.6	4.1	1243	8	US-10-425-115-172717	Sequence 172717,
c	44	113.6	4.1	1300	7	US-10-668-749A-1	Sequence 1, Appli
	45	113.2	4.1	1121	8	US-10-425-115-115706	Sequence 115706,

ALIGNMENTS

RESULT 1
US-10-677-254-2
; Sequence 2, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2783
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-2

Query Match 100.0%; Score 2783; DB 8; Length 2783;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2783; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GCAGTAAATTGATTCAAACTGAAATCACTGCAAAATGATTCTAATAGTAAATGCAAATTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCAGTAAATTGATTCAAACTGAAATCACTGCAAAATGATTCTAATAGTAAATGCAAATTC 60

Qy         61 TGAGCAAATGACTGAATATACACTCTCCGGCCACTTCATTAGGTACACCTGTCCAACTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGAGCAAATGACTGAATATACACTCTCCGGCCACTTCATTAGGTACACCTGTCCAACTGC 120

Qy        121 TCATTAATGCAAATTTCTAATCAACCACTCACATGGCAGCAACTCAATGCATTAAGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCATTAATGCAAATTTCTAATCAACCACTCACATGGCAGCAACTCAATGCATTAAGGTAC 180

Qy        181 GTAGACATGGTCAAGACGATCTGCTGCAGTTCAAACTGAGCATCAGAATGGGGAAGGAAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTAGACATGGTCAAGACGATCTGCTGCAGTTCAAACTGAGCATCAGAATGGGGAAGGAAG 240

Qy        241 AGGATTTCAGTGACTTTGAACGAGGCATGGTTGTTGCTGCCGGATGGGCTGCTCTGAGTA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGGATTTCAGTGACTTTGAACGAGGCATGGTTGTTGCTGCCGGATGGGCTGCTCTGAGTA 300

Qy        301 TTTCAGAAACTGCTGATCTTCAGGGATTTTCACGCACAACCATCTCTAGGGTTTACAGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 15932.3 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-2
Perfect score: 2783
Sequence: 1 gcagtaaattgattcaaact.....gttgagcttctccagaaagc 2783

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	505.4	18.2	811	10	BX137211	BX137211 Danio rer
c	2	482	17.3	662	3	BI891633	BI891633 ZF637-3-0
	3	475.8	17.1	759	10	BX221257	BX221257 Danio rer
	4	473.8	17.0	767	10	BX186579	BX186579 Danio rer
	5	473.8	17.0	815	10	BX201471	BX201471 Danio rer
c	6	468.2	16.8	1019	11	CNS04H1S	AL290377 Tetraodon
c	7	464.6	16.7	784	7	CK142722	CK142722 AGENCOURT
	8	457.2	16.4	725	10	BX215917	BX215917 Danio rer
	9	454	16.3	848	10	BX237967	BX237967 Danio rer
	10	452.6	16.3	795	10	BX246833	BX246833 Danio rer
	11	440.2	15.8	1096	11	CNS05BMU	AL330015 Tetraodon
c	12	439.4	15.8	851	6	CA475175	CA475175 AGENCOURT
c	13	437.8	15.7	640	7	CO354767	CO354767 DR_ATE_PL
	14	436.2	15.7	743	10	BX128033	BX128033 Danio rer
c	15	435.4	15.6	829	10	BX175361	BX175361 Danio rer
c	16	433.4	15.6	746	10	BX136809	BX136809 Danio rer
	17	431	15.5	759	10	BX243117	BX243117 Danio rer
c	18	430.6	15.5	656	10	BX168493	BX168493 Danio rer
	19	429	15.4	811	10	BX160302	BX160302 Danio rer
	20	428.2	15.4	641	11	DR20I21S	AL736393 Danio rer
	21	427.8	15.4	859	11	CNS03DSR	AL239508 Tetraodon
c	22	426.6	15.3	685	10	BX153476	BX153476 Danio rer
	23	426.4	15.3	771	10	BX242795	BX242795 Danio rer
	24	425.2	15.3	814	10	BX247334	BX247334 Danio rer
	25	422.4	15.2	642	10	BX153159	BX153159 Danio rer
	26	422.4	15.2	772	10	BX213642	BX213642 Danio rer
c	27	421.4	15.1	747	10	BX241629	BX241629 Danio rer
	28	416.6	15.0	632	10	BX125722	BX125722 Danio rer
	29	414.6	14.9	799	10	BX238228	BX238228 Danio rer
c	30	412.8	14.8	793	10	BX159318	BX159318 Danio rer
c	31	409.8	14.7	680	10	BX181467	BX181467 Danio rer
c	32	409.8	14.7	817	10	BX171925	BX171925 Danio rer
c	33	408.8	14.7	703	10	BX229586	BX229586 Danio rer
c	34	407.8	14.7	683	10	BX180634	BX180634 Danio rer
c	35	407.8	14.7	789	10	BX179889	BX179889 Danio rer
	36	407.6	14.6	690	10	BX132285	BX132285 Danio rer
c	37	407.4	14.6	814	10	BX215696	BX215696 Danio rer
	38	407	14.6	797	10	BX230975	BX230975 Danio rer
c	39	406.8	14.6	696	10	BX240939	BX240939 Danio rer
	40	404.6	14.5	853	10	BX180521	BX180521 Danio rer
c	41	402.2	14.5	581	11	DR102L21S	AL973497 Danio rer
c	42	401.6	14.4	646	11	DR34C7S	AL976117 Danio rer
c	43	399.4	14.4	693	10	BX164828	BX164828 Danio rer
	44	398.8	14.3	801	10	BX167583	BX167583 Danio rer
c	45	397.6	14.3	752	10	BX171036	BX171036 Danio rer

ALIGNMENTS

RESULT 1
BX137211
LOCUS BX137211 811 bp DNA linear GSS 28-JAN-2003
DEFINITION Danio rerio genomic clone DKEY-98F14, genomic survey sequence.
ACCESSION BX137211
VERSION BX137211.1 GI:27968523
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 811)
AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the SP6 end of BAC 98F14. 98F14 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES Location/Qualifiers
source 1. .811
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-98F14"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
ORIGIN

Query Match 18.2%; Score 505.4; DB 10; Length 811;
Best Local Similarity 93.8%; Pred. No. 9.1e-76;
Matches 549; Conservative 0; Mismatches 31; Indels 5; Gaps 2;

```
Qy         77 TATACACTCTCCGGCCACTTCATTAGGTACACCTGTCCAACTGCTCATTAATGCAAATTT 136
              ||||||||| |||||||||||||||||||| |||||||||| |||| |||||||
Db         30 TATACACTCAACGGCCACTTCATTAGGTACACCTCTCCAACTGCTCGTTAACTCAAATTT 89

Qy        137 CTAATCAACCACTCACATGGCAGCAACTCAATGCATTAAGGTACGTAGACATGGTCAAGA 196
              ||||||| ||| |||||||||||||| |||| |||||| ||| | ||||||||||||||||
Db         90 CTAATCAGCCAATCACATGGCAGCAGCTCACTGCATTTAGGCATGTAGACATGGTCAAGA 149

Qy        197 CGATCTGCTGCAGTTCAAACTGAGCATCAGAATGGGGAAGGAAGAGGATTTCAGTGACTT 256
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:12:08 ; Search time 386.414 Seconds
(without alignments)
4495.063 Million cell updates/sec

Title: US-10-717-573-1
Perfect score: 435
Sequence: 1 gtatacaatgacttgcctaa.....aaaattgagtaaatccaagg 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		51.8	11.9	139054	14	US-11-121-086-96	Sequence 96, Appl
2		49.4	11.4	628	6	US-09-925-065A-793033	Sequence 793033,
3	c	49.4	11.4	633	6	US-09-925-065A-795408	Sequence 795408,
4	c	48	11.0	557	6	US-09-925-065A-427734	Sequence 427734,
5		47.8	11.0	628	6	US-09-925-065A-793034	Sequence 793034,
6	c	47.8	11.0	633	6	US-09-925-065A-795407	Sequence 795407,
7	c	47.2	10.9	587	6	US-09-925-065A-610490	Sequence 610490,
8		46.8	10.8	674	10	US-10-301-480-580603	Sequence 580603,
9		46.8	10.8	674	10	US-10-301-480-1194012	Sequence 1194012,
10		46.8	10.8	736	10	US-10-301-480-552955	Sequence 552955,
11		46.8	10.8	736	10	US-10-301-480-1166364	Sequence 1166364,
12	c	46.2	10.6	98716	8	US-10-995-561-13331	Sequence 13331, A
13		45.4	10.4	1065	9	US-10-301-480-93483	Sequence 93483, A
14		45.4	10.4	1065	10	US-10-301-480-706892	Sequence 706892,
15	c	45.4	10.4	5006	11	US-11-202-731-7	Sequence 7, Appli
16		45.4	10.4	236246	9	US-10-330-773-567	Sequence 567, App
17	c	45.2	10.4	990	10	US-10-301-480-568794	Sequence 568794,
18	c	45.2	10.4	990	10	US-10-301-480-1182203	Sequence 1182203,
19		45	10.3	606	6	US-09-925-065A-805604	Sequence 805604,
20		45	10.3	607	6	US-09-925-065A-807495	Sequence 807495,
21	c	44.8	10.3	534	10	US-10-301-480-490988	Sequence 490988,
22	c	44.8	10.3	534	10	US-10-301-480-1104397	Sequence 1104397,
23	c	44.8	10.3	1457619	14	US-11-098-686-8739	Sequence 8739, Ap
24		44.4	10.2	529	6	US-09-925-065A-387426	Sequence 387426,
25		44.4	10.2	529	6	US-09-925-065A-387427	Sequence 387427,
26	c	44.4	10.2	532	6	US-09-925-065A-301102	Sequence 301102,
27		44.4	10.2	542	6	US-09-925-065A-864085	Sequence 864085,
28	c	44.4	10.2	624	6	US-09-925-065A-103837	Sequence 103837,
29		44.4	10.2	628	6	US-09-925-065A-873640	Sequence 873640,
30		44.4	10.2	669	6	US-09-925-065A-9048	Sequence 9048, Ap
31		44.4	10.2	669	6	US-09-925-065A-9049	Sequence 9049, Ap
32		44.4	10.2	669	6	US-09-925-065A-9050	Sequence 9050, Ap
33		44.4	10.2	669	9	US-10-301-480-110285	Sequence 110285,
34		44.4	10.2	669	9	US-10-301-480-110286	Sequence 110286,
35		44.4	10.2	669	9	US-10-301-480-110287	Sequence 110287,
36		44.4	10.2	669	10	US-10-301-480-723694	Sequence 723694,
37		44.4	10.2	669	10	US-10-301-480-723695	Sequence 723695,
38		44.4	10.2	669	10	US-10-301-480-723696	Sequence 723696,
39	c	44.2	10.2	633	10	US-10-301-480-589139	Sequence 589139,
40	c	44.2	10.2	633	10	US-10-301-480-589140	Sequence 589140,
41	c	44.2	10.2	633	10	US-10-301-480-1202548	Sequence 1202548,
42	c	44.2	10.2	633	10	US-10-301-480-1202549	Sequence 1202549,
43		44.2	10.2	1096	6	US-09-925-065A-57855	Sequence 57855, A
44		44.2	10.2	1096	9	US-10-301-480-159093	Sequence 159093,
45		44.2	10.2	1096	10	US-10-301-480-772502	Sequence 772502,

ALIGNMENTS

RESULT 1
US-11-121-086-96
; Sequence 96, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 96
; LENGTH: 139054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-96

Query Match 11.9%; Score 51.8; DB 14; Length 139054;
Best Local Similarity 49.5%; Pred. No. 9.1;
Matches 160; Conservative 0; Mismatches 162; Indels 1; Gaps 1;

```
Qy      105 TATCTAGTCTAATATTATTGACTGTCATCATGGCAAAGATAAAATAAATCAGTTATTAAA 164
            ||| || | ||  |||||  | | | || ||   | |     | ||      | |||||
Db    43286 TATATAATATATAATTATATAATATAATAATAATATATTATTACTATTAATATAATTAAT 43345

Qy      165 ACTATTATGATTAGAAATGTGCTGAAACAATCTGCTCTCCGATAAACAGAAATTGAACAA 224
            | |||||| |||| |  |     |  || | | |     | | ||||     ||||| ||  |
Db    43346 AATATTATAATTATATTTAAATTATAAAATTATAAATTTC-ATAATTTAAAATTAAATTA 43404

Qy      225 AATAAACAGGGGGGCTAATAAATTTAAGGGGTTAAATAATTCTGATTGCAAAAAAAATGA 284
            ||| |  |          |   |||||||     |  || |  | | |||  |  | | ||
Db    43405 AATTATAAAAATTTAAATGTAATTTAAAATATATAAAATATATAATTTAATTATACATTC 43464

Qy      285 TGTCTGCAAAACTGTTGCAAATAATTTATTTGTGTTGATTTTAAGCAAACAAATTAAATT 344
            | | |  |       ||| |  ||| |   ||  | |     |   |||| ||
Db    43465 CATATACTTTATATAATTTAATCAACTATATAATTTATATATTTAATACATAATTTAAAA 43524
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 06:06:01 ; Search time 507.148 Seconds
(without alignments)
7092.959 Million cell updates/sec

Title: US-10-717-573-1
Perfect score: 435
Sequence: 1 gtatacaatgacttgcctaa.....aaaattgagtaaatccaagg 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	435	100.0	435	8	US-10-677-254-1	Sequence 1, Appli
	2	435	100.0	435	8	US-10-717-573-1	Sequence 1, Appli
	3	435	100.0	480	8	US-10-677-254-30	Sequence 30, Appl
	4	435	100.0	480	8	US-10-717-573-30	Sequence 30, Appl
	5	435	100.0	2033	8	US-10-677-254-3	Sequence 3, Appli
	6	435	100.0	2033	8	US-10-717-573-3	Sequence 3, Appli
	7	435	100.0	2783	8	US-10-677-254-2	Sequence 2, Appli
	8	435	100.0	2783	8	US-10-717-573-2	Sequence 2, Appli
c	9	167.8	38.6	3003	9	US-10-511-362-9	Sequence 9, Appli
	10	163.6	37.6	13382	8	US-10-612-594-4	Sequence 4, Appli
c	11	149.2	34.3	5563	5	US-10-136-734-26	Sequence 26, Appl
c	12	144	33.1	7495	7	US-10-742-828-5	Sequence 5, Appli
c	13	144	33.1	7508	7	US-10-742-828-4	Sequence 4, Appli
c	14	124.4	28.6	13382	8	US-10-612-594-4	Sequence 4, Appli
c	15	86.6	19.9	71843	9	US-10-488-292-3	Sequence 3, Appli
c	16	64.6	14.9	435	8	US-10-677-254-1	Sequence 1, Appli
c	17	64.6	14.9	435	8	US-10-717-573-1	Sequence 1, Appli
c	18	64.6	14.9	480	8	US-10-677-254-30	Sequence 30, Appl
c	19	64.6	14.9	480	8	US-10-717-573-30	Sequence 30, Appl
c	20	64.6	14.9	2033	8	US-10-677-254-3	Sequence 3, Appli
c	21	64.6	14.9	2033	8	US-10-717-573-3	Sequence 3, Appli
c	22	64.6	14.9	2783	8	US-10-677-254-2	Sequence 2, Appli
c	23	64.6	14.9	2783	8	US-10-717-573-2	Sequence 2, Appli
	24	55.8	12.8	517	7	US-10-021-323-11054	Sequence 11054, A
c	25	55.4	12.7	9547	6	US-10-311-455-1477	Sequence 1477, Ap
c	26	55.2	12.7	7346	6	US-10-311-455-318	Sequence 318, App
c	27	52.6	12.1	3673778	6	US-10-312-841-2	Sequence 2, Appli
c	28	52.4	12.0	16439	6	US-10-311-455-860	Sequence 860, App
c	29	51.8	11.9	50000	8	US-10-706-635-23	Sequence 23, Appl
	30	51.8	11.9	3673778	6	US-10-312-841-2	Sequence 2, Appli
c	31	51.4	11.8	11745	6	US-10-240-453-206	Sequence 206, App
c	32	51	11.7	8076	7	US-10-257-166-36	Sequence 36, Appl
c	33	51	11.7	8136	6	US-10-311-455-528	Sequence 528, App
c	34	51	11.7	8136	7	US-10-257-166-38	Sequence 38, Appl
c	35	50.8	11.7	14095	6	US-10-311-455-450	Sequence 450, App
	36	50.6	11.6	6059	6	US-10-311-455-1453	Sequence 1453, Ap
c	37	50.6	11.6	15416	6	US-10-311-455-2204	Sequence 2204, Ap
c	38	50.6	11.6	15416	7	US-10-221-613-418	Sequence 418, App
	39	50.4	11.6	368	7	US-10-021-323-5024	Sequence 5024, Ap
c	40	50.4	11.6	7676	6	US-10-240-485-151	Sequence 151, App
c	41	50	11.5	7076	6	US-10-311-455-2117	Sequence 2117, Ap
c	42	49.8	11.4	13449	6	US-10-311-455-1357	Sequence 1357, Ap
c	43	49.8	11.4	3673778	6	US-10-312-841-1	Sequence 1, Appli
c	44	49.6	11.4	6631	6	US-10-240-453-214	Sequence 214, App
c	45	49.6	11.4	200000	7	US-10-672-764A-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-677-254-1
; Sequence 1, Application US/10677254
; Publication No. US20040209279A1
; GENERAL INFORMATION:
; APPLICANT: WU, Jen-Leih
; APPLICANT: HER, Guor Mour
; TITLE OF INVENTION: EXPRESSION CONTROL SEQUENCES MODULATING LIVER FATTY ACID BINDING
; TITLE OF INVENTION: PROTEIN (L-FABP) GENE AND TRANSGENIC FISH COMPRISING THEM
; FILE REFERENCE: 33151-188802
; CURRENT APPLICATION NUMBER: US/10/677,254
; CURRENT FILING DATE: 2003-10-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-677-254-1

Query Match 100.0%; Score 435; DB 8; Length 435;
Best Local Similarity 100.0%; Pred. No. 8.7e-76;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GTATACAATGACTTGCCTAATTACCCTAACCTGCCTAGTTACCCTAATTAACCTAGTTAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTATACAATGACTTGCCTAATTACCCTAACCTGCCTAGTTACCCTAATTAACCTAGTTAA 60

Qy         61 GCCTTTAAATGTCACTTTAAGCTGTATAGAAGTGTCTTGAAGAATATCTAGTCTAATATT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCTTTAAATGTCACTTTAAGCTGTATAGAAGTGTCTTGAAGAATATCTAGTCTAATATT 120

Qy        121 ATTGACTGTCATCATGGCAAAGATAAAATAAATCAGTTATTAAAACTATTATGATTAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTGACTGTCATCATGGCAAAGATAAAATAAATCAGTTATTAAAACTATTATGATTAGAA 180

Qy        181 ATGTGCTGAAACAATCTGCTCTCCGATAAACAGAAATTGAACAAAATAAACAGGGGGGCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTGCTGAAACAATCTGCTCTCCGATAAACAGAAATTGAACAAAATAAACAGGGGGGCT 240

Qy        241 AATAAATTTAAGGGGTTAAATAATTCTGATTGCAAAAAAAATGATGTCTGCAAAACTGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AATAAATTTAAGGGGTTAAATAATTCTGATTGCAAAAAAAATGATGTCTGCAAAACTGTT 300

Qy        301 GCAAATAATTTATTTGTGTTGATTTTAAGCAAACAAATTAAATTTAATAAAATACAACTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:58:23 ; Search time 86.8538 Seconds
(without alignments)
8902.774 Million cell updates/sec

Title: US-10-717-573-1
Perfect score: 435
Sequence: 1 gtatacaatgacttgcctaa.....aaaattgagtaaatccaagg 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	51.8	11.9	50000	3	US-09-662-254B-23	Sequence 23, Appl
	2	49.4	11.4	108310	3	US-09-949-016-16366	Sequence 16366, A
c	3	48	11.0	50000	3	US-09-662-254B-25	Sequence 25, Appl
c	4	46.2	10.6	264665	3	US-09-949-016-13747	Sequence 13747, A
c	5	45.8	10.5	147382	3	US-09-949-016-14624	Sequence 14624, A
c	6	45.4	10.4	18651	3	US-09-949-002-592	Sequence 592, App
c	7	45.4	10.4	18682	3	US-09-949-002-786	Sequence 786, App
c	8	45.4	10.4	29717	3	US-09-949-016-16284	Sequence 16284, A
c	9	45.4	10.4	60376	3	US-09-949-016-12423	Sequence 12423, A
c	10	45.2	10.4	263693	3	US-09-949-016-12386	Sequence 12386, A
c	11	45.2	10.4	263694	3	US-09-949-016-16915	Sequence 16915, A
	12	45	10.3	663	3	US-08-998-416-191	Sequence 191, App
	13	45	10.3	2244	3	US-09-601-198-149	Sequence 149, App
c	14	44.6	10.3	4673	2	US-07-638-431-1	Sequence 1, Appli
c	15	44.6	10.3	4673	6	PCT-US92-00018-1	Sequence 1, Appli
	16	44.6	10.3	187169	3	US-09-949-016-12776	Sequence 12776, A
	17	44.6	10.3	191569	3	US-09-949-016-15940	Sequence 15940, A
	18	44.4	10.2	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	19	44.4	10.2	20674	3	US-09-641-638-651	Sequence 651, App
c	20	44.4	10.2	20674	3	US-10-170-097-651	Sequence 651, App
	21	44.4	10.2	29927	3	US-09-949-016-11814	Sequence 11814, A
	22	44.4	10.2	29927	3	US-09-949-016-17474	Sequence 17474, A
	23	44.4	10.2	29927	3	US-09-949-016-17475	Sequence 17475, A
	24	44.4	10.2	37802	3	US-09-949-016-12639	Sequence 12639, A
c	25	44.2	10.2	662	3	US-08-998-416-185	Sequence 185, App
c	26	44.2	10.2	665	3	US-08-998-416-937	Sequence 937, App
c	27	44.2	10.2	701	3	US-08-998-416-701	Sequence 701, App
c	28	44.2	10.2	711	3	US-08-998-416-786	Sequence 786, App
c	29	44.2	10.2	724	3	US-08-998-416-683	Sequence 683, App
c	30	44.2	10.2	732	3	US-08-998-416-1036	Sequence 1036, Ap
c	31	44.2	10.2	828	3	US-08-998-416-538	Sequence 538, App
c	32	44.2	10.2	834	3	US-08-998-416-305	Sequence 305, App
c	33	43.8	10.1	6881	3	US-09-949-016-17181	Sequence 17181, A
	34	43.8	10.1	15220	3	US-09-949-016-16311	Sequence 16311, A
	35	43.6	10.0	1039	3	US-09-902-540-1280	Sequence 1280, Ap
c	36	43.6	10.0	96922	3	US-09-949-016-17061	Sequence 17061, A
	37	43.4	10.0	696	3	US-09-248-796A-11043	Sequence 11043, A
c	38	43.4	10.0	782	3	US-08-998-416-224	Sequence 224, App
c	39	43.2	9.9	32721	3	US-09-949-016-14100	Sequence 14100, A
c	40	43.2	9.9	45138	3	US-09-949-016-13027	Sequence 13027, A
	41	43	9.9	860	3	US-08-998-416-287	Sequence 287, App
c	42	43	9.9	1141	3	US-09-806-708B-22	Sequence 22, Appl
c	43	43	9.9	16062	3	US-09-949-016-13181	Sequence 13181, A
c	44	42.8	9.8	601	3	US-09-949-016-81304	Sequence 81304, A
c	45	42.8	9.8	27757	3	US-09-949-016-12407	Sequence 12407, A

ALIGNMENTS

RESULT 1
US-09-662-254B-23/c
; Sequence 23, Application US/09662254B
; Patent No. 6933145
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Li, Yi
; APPLICANT: Bawden, Alison Louise
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologou
; TITLE OF INVENTION: Vertebrate Cells
; FILE REFERENCE: UF-221C1XC1
; CURRENT APPLICATION NUMBER: US/09/662,254B
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Amsacta moorei entomopoxvirus
US-09-662-254B-23

Query Match 11.9%; Score 51.8; DB 3; Length 50000;
Best Local Similarity 51.3%; Pred. No. 0.018;
Matches 172; Conservative 0; Mismatches 157; Indels 6; Gaps 2;

```
Qy      104 ATATCTAGTCTAATATTATTGACTGTCATCATGGCAAAGATAAAATAAATCAGTTATTAA 163
            |||| || |  |||||  |||      ||   | ||| ||||  |||| | |  |
Db    16973 ATATATAATAATATATTTATGATACCATTCTATGGAAAAATAAATAAAATAAATATTATT 16914

Qy      164 AACTATTATGATTAGAAATGTGCTGAAACAATCTGCTCTCCGATAAACAGAAATT----G 219
            ||  || || || | || | |    | |  || |  |      |||||| | |||
Db    16913 AATAATGATCATAATAATTATATAAATAGTATTTTATTAAAAATAAACAAATATTTTGAT 16854

Qy      220 AACAAAATAAACAGGGGGGCTAATAAATTTAAGGGGTTAAATAATTCTGATTGCAAAAAA 279
            || |||||| | |      |  |||| ||| |      | ||  | | ||   ||  ||
Db    16853 AAAAAAATAGATAATAATGTATATAATTTTGACACAAATATTATATGTAATATAAATGAA 16794

Qy      280 AATGATGTCTGCAAAACTGTTGCAAATAATTTATTTGTGTTGATTTTAAGCAAACAAATT 339
            ||||||  |  ||||  |  |  |  ||||  || | ||    |  |  | | ||||
Db    16793 AATGATATA--CAAATATTATATTATAAATTAGATTATTTTATACTCGAATATAAAAATA 16736

Qy      340 AAATTTAATAAAATACAACTTAATCTGTTTGTTTAAATTCAGCCCTAATAAATTGTTTAC 399
              | ||  ||||||  |  ||  || || | |||| |       |  |||||| ||
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:16:37 ; Search time 356.027 Seconds
(without alignments)
8143.032 Million cell updates/sec

Title: US-10-717-573-1
Perfect score: 435
Sequence: 1 gtatacaatgacttgcctaa.....aaaattgagtaaatccaagg 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	435	100.0	435	13	ADT08242	Adt08242 Zebrafish
	2	435	100.0	435	13	ADT89050	Adt89050 Zebrafish
	3	435	100.0	480	13	ADT08271	Adt08271 Zebrafish
	4	435	100.0	480	13	ADT89079	Adt89079 Zebrafish
	5	435	100.0	2033	13	ADT08244	Adt08244 Zebrafish
	6	435	100.0	2033	13	ADT89052	Adt89052 Zebrafish
	7	435	100.0	2783	13	ADT08243	Adt08243 Zebrafish
	8	435	100.0	2783	13	ADT89051	Adt89051 Zebrafish
	9	435	100.0	2960	13	ADT89080	Adt89080 Zebrafish
	10	176.2	40.5	78064	13	ADS17402	Ads17402 Nucleotid
c	11	167.8	38.6	3003	10	ADF18692	Adf18692 Zebrafish
	12	163.6	37.6	13382	14	ADW44488	Adw44488 Zebrafish
c	13	149.2	34.3	5563	2	AAX08941	Aax08941 GATA-1 pr
c	14	147.6	33.9	78064	13	ADS17402	Ads17402 Nucleotid
c	15	144	33.1	7495	13	ADR30815	Adr30815 Zebrafish
c	16	144	33.1	7508	13	ADR30814	Adr30814 Zebrafish
c	17	124.4	28.6	13382	14	ADW44488	Adw44488 Zebrafish
c	18	86.6	19.9	71843	8	ACC79619	Acc79619 Zebrafish
c	19	64.6	14.9	435	13	ADT08242	Adt08242 Zebrafish
c	20	64.6	14.9	435	13	ADT89050	Adt89050 Zebrafish
c	21	64.6	14.9	480	13	ADT08271	Adt08271 Zebrafish
c	22	64.6	14.9	480	13	ADT89079	Adt89079 Zebrafish
c	23	64.6	14.9	2033	13	ADT08244	Adt08244 Zebrafish
c	24	64.6	14.9	2033	13	ADT89052	Adt89052 Zebrafish
c	25	64.6	14.9	2783	13	ADT08243	Adt08243 Zebrafish
c	26	64.6	14.9	2783	13	ADT89051	Adt89051 Zebrafish
c	27	64.6	14.9	2960	13	ADT89080	Adt89080 Zebrafish
c	28	62	14.3	98800	12	ADN06353_3	Continuation (4 of
c	29	62	14.3	98800	13	ADS94372_3	Continuation (4 of
	30	55.8	12.8	517	13	ACN56273	Acn56273 Cotton an
c	31	55.4	12.7	9547	6	ABL33504	Abl33504 Human imm
c	32	55.2	12.7	7346	6	ABL32345	Abl32345 Human imm
c	33	52.4	12.0	16439	6	ABL32887	Abl32887 Human imm
c	34	51.8	11.9	50000	6	ABL55643	Abl55643 AmEPV gen
c	35	51.4	11.8	11745	6	ABK28332	Abk28332 DNA trans
c	36	51	11.7	8076	6	ABK39955	Abk39955 Human che
c	37	51	11.7	8136	6	ABK39957	Abk39957 Human che
c	38	51	11.7	8136	6	ABL32555	Abl32555 Human imm
c	39	51	11.7	17897	10	ADB54178	Adb54178 Pretreate
c	40	51	11.7	17897	13	ADS89328	Ads89328 Oligonucl
c	41	50.8	11.7	14095	6	ABL32477	Abl32477 Human imm
	42	50.6	11.6	6059	6	ABL33480	Abl33480 Human imm
c	43	50.6	11.6	15416	6	ABL34231	Abl34231 Human imm
c	44	50.6	11.6	15416	6	ABK31527	Abk31527 Signal tr
c	45	50.6	11.6	15416	6	ABL70498	Abl70498 Chemicall

ALIGNMENTS

RESULT 1
ADT08242
ID ADT08242 standard; DNA; 435 BP.
XX
AC ADT08242;
XX
DT 13-JAN-2005 (first entry)
XX
DE Zebrafish L-FABP upstream region -1983 to -1504.
XX
KW Zebrafish; ds; liver fatty acid binding protein; L-FABP;
KW liver regulatory element; LR; transgenic; HFH(1); HFH(2); HNF-1alpha;
KW HNF-3 beta; PDX1; PDX2; green fluorescent protein; GFP;
KW liver development; liver disease; liver necrosis; liver cancer.
XX
OS Danio rerio.
XX
FH Key Location/Qualifiers
FT protein_bind 48. .68
FT /*tag= a
FT /bound_moiety= "PDX1"
FT protein_bind 75. .94
FT /*tag= b
FT /bound_moiety= "PDX1"
FT protein_bind 346. .360
FT /*tag= c
FT /bound_moiety= "HNF-1alpha"
FT protein_bind 365. .380
FT /*tag= d
FT /bound_moiety= "HNF-3beta"
XX
PN US2004209833-A1.
XX
PD 21-OCT-2004.
XX
PF 21-NOV-2003; 2003US-00717573.
XX
PR 16-APR-2003; 2003US-0463035P.
PR 27-MAY-2003; 2003US-0473210P.
XX
PA (WUJJ/) WU J.
PA (HERG/) HER G M.

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:54:26 ; Search time 2490.32 Seconds
(without alignments)
8172.589 Million cell updates/sec

Title: US-10-717-573-1
Perfect score: 435
Sequence: 1 gtatacaatgacttgcctaa.....aaaattgagtaaatccaagg 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	204	46.9	738	10	BX240588	BX240588 Danio rer
c	2	204	46.9	823	10	BX208028	BX208028 Danio rer
c	3	204	46.9	838	10	BX132903	BX132903 Danio rer
c	4	191.2	44.0	677	8	DN901058	DN901058 naq14d10.
c	5	190	43.7	802	1	AL719686	AL719686 AL719686
c	6	189	43.4	684	10	BX148326	BX148326 Danio rer
c	7	187.2	43.0	765	10	BX133288	BX133288 Danio rer
	8	187	43.0	817	10	BX209382	BX209382 Danio rer
	9	186.8	42.9	684	1	AL719627	AL719627 AL719627
	10	186	42.8	477	10	BX165718	BX165718 Danio rer
	11	185.8	42.7	676	10	BX136825	BX136825 Danio rer
c	12	185.4	42.6	480	1	AI545476	AI545476 fb81h04.x
	13	185.4	42.6	500	6	CD581432	CD581432 RK012A4H1
c	14	185	42.5	529	10	BX206150	BX206150 Danio rer
c	15	184.8	42.5	762	10	BX218760	BX218760 Danio rer
c	16	184.6	42.4	731	10	BX157770	BX157770 Danio rer
c	17	184	42.3	705	10	BX157281	BX157281 Danio rer
c	18	183.6	42.2	534	3	BI877248	BI877248 fl82f12.y
	19	183.6	42.2	822	10	BX161705	BX161705 Danio rer
c	20	183	42.1	741	10	BX139380	BX139380 Danio rer
	21	183	42.1	777	10	BX153299	BX153299 Danio rer
c	22	182.8	42.0	778	10	BX147912	BX147912 Danio rer
c	23	182.8	42.0	802	10	BX158185	BX158185 Danio rer
	24	182.4	41.9	647	10	BX199272	BX199272 Danio rer
c	25	182.2	41.9	712	10	BX189345	BX189345 Danio rer
	26	182.2	41.9	797	10	BX221296	BX221296 Danio rer
	27	182	41.8	525	3	BM572872	BM572872 fx50g08.y
	28	182	41.8	849	8	DN858051	DN858051 naa21e09.
	29	181.8	41.8	548	10	BX130901	BX130901 Danio rer
	30	181.8	41.8	554	1	AI588386	AI588386 fc01b09.x
c	31	181.4	41.7	766	10	BX228472	BX228472 Danio rer
c	32	181.2	41.7	659	10	BX163107	BX163107 Danio rer
c	33	181.2	41.7	735	10	BX172233	BX172233 Danio rer
c	34	181	41.6	754	8	DR728618	DR728618 AGENCOURT
c	35	180.6	41.5	629	10	BX218791	BX218791 Danio rer
	36	180.6	41.5	793	7	CK707383	CK707383 ZF101-P00
	37	180.4	41.5	623	1	AL720634	AL720634 AL720634
	38	180.2	41.4	515	3	BI705881	BI705881 fp97f06.y
c	39	180.2	41.4	657	10	BX137240	BX137240 Danio rer
	40	180	41.4	615	10	BX137736	BX137736 Danio rer
c	41	180	41.4	712	10	BX188692	BX188692 Danio rer
	42	180	41.4	723	10	BX225086	BX225086 Danio rer
	43	180	41.4	842	10	BX212779	BX212779 Danio rer
c	44	179.8	41.3	743	10	BX198263	BX198263 Danio rer
	45	179.6	41.3	712	10	BX123984	BX123984 Danio rer

ALIGNMENTS

RESULT 1
BX240588/c
LOCUS BX240588 738 bp DNA linear GSS 29-JAN-2003
DEFINITION Danio rerio genomic clone DKEY-288B14, genomic survey sequence.
ACCESSION BX240588
VERSION BX240588.1 GI:28162922
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 738)
AUTHORS Humphray,S.J., Huckle,E. and Durham,J.L.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
COMMENT This sequence was generated from the T7 end of BAC 288B14. 288B14 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
FEATURES Location/Qualifiers
source 1. .738
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-288B14"
/tissue_type="Testis"
/note="vector pIndigoBAC-536"
ORIGIN

Query Match 46.9%; Score 204; DB 10; Length 738;
Best Local Similarity 90.9%; Pred. No. 4.1e-29;
Matches 229; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

```
Qy          2 TATACAATGACTTGCCTAATTACCCTAACCTGCCTAGTTACCCTAATTAACCTAGTTAAG 61
              |||||| |||||||||||||||||||||||||||||| |||||||||||||||||||||
Db        473 TATACAATAACTTGCCTAATTACCCTAACCTGCCTAGTTAACCTAATTAACCTAGTTAAG 414

Qy         62 CCTTTAAATGTCACTTTAAGCTGTATAGAAGTGTCTTGAAGAATATCTAGTCTAATATTA 121
              |||||||||| |||| |||||||||||||||||||| |||||||||||||| || ||||
Db        413 CCTTTAAATGCCACTCTAAGCTGTATAGAAGTGTCTTAAAGAATATCTAGTCAAACATTA 354

Qy        122 TTGACTGTCATCATGGCAAAGATAAAATAAATCAGTTATTAAAACTATTATGATTAGAAA 181
```

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 05:44:25 ; Search time 2587.9 Seconds
(without alignments)
9554.811 Million cell updates/sec

Title: US-10-717-573-1
Perfect score: 435
Sequence: 1 gtatacaatgacttgcctaa.....aaaattgagtaaatccaagg 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		435	100.0	2960	5	AF512998	AF512998 Danio rer
c 2		420.6	96.7	178271	5	CR293507	CR293507 Zebrafish
3		223.2	51.3	85762	5	CR388368	CR388368 Zebrafish
4		218	50.1	80017	5	AL845372	AL845372 Zebrafish
c 5		218	50.1	150673	14	CR361557	CR361557 Danio rer
c 6		208.8	48.0	137636	14	CR788291	CR788291 Danio rer
c 7		206.8	47.5	153267	14	CR354434	CR354434 Danio rer
c 8		206.2	47.4	191769	14	CR933561	CR933561 Danio rer
c 9		205.8	47.3	169046	5	AL928828	AL928828 Zebrafish
10		204	46.9	162436	5	AL929535	AL929535 Zebrafish
c 11		203.8	46.9	171208	5	BX296552	BX296552 Zebrafish
c 12		203	46.7	231303	5	BX649405	BX649405 Zebrafish
c 13		202.2	46.5	185384	14	CR391914	CR391914 Danio rer
14		202.2	46.5	203371	14	AC139623	AC139623 Danio rer
c 15		202	46.4	154824	5	BX323864	BX323864 Zebrafish
16		202	46.4	163815	5	CR392361	CR392361 Zebrafish
17		202	46.4	192644	14	CR762383	CR762383 Danio rer
c 18		202	46.4	221617	5	BX530018	BX530018 Zebrafish
c 19		201.6	46.3	156150	5	BX322540	BX322540 Zebrafish
c 20		201.2	46.3	162129	5	CR385035	CR385035 Zebrafish
21		201.2	46.3	228771	14	CR855129	CR855129 Danio rer
c 22		201.2	46.3	256437	5	BX664629	BX664629 Zebrafish
23		201.2	46.3	304914	14	BX942830	BX942830 Danio rer
c 24		200.8	46.2	222975	14	CR848050	CR848050 Danio rer
c 25		199.8	45.9	190968	5	BX465217	BX465217 Zebrafish
c 26		199.4	45.8	192117	5	BX663603	BX663603 Zebrafish
c 27		199.2	45.8	216817	14	CR855117	CR855117 Danio rer
28		199.2	45.8	222979	14	CR931761	CR931761 Danio rer
29		199	45.7	137477	5	BX004882	BX004882 Zebrafish
c 30		198.8	45.7	114105	14	CR354589	CR354589 Danio rer
c 31		198.6	45.7	160087	5	BX004867	BX004867 Zebrafish
c 32		198.4	45.6	173914	5	BX279525	BX279525 Zebrafish
c 33		198.2	45.6	147179	5	CR384061	CR384061 Zebrafish
34		198.2	45.6	150490	14	CR450768	CR450768 Danio rer
35		198	45.5	215891	5	AL928692	AL928692 Zebrafish
36		197.8	45.5	98234	5	BX001026	BX001026 Zebrafish
c 37		197.4	45.4	149630	14	CR628386	CR628386 Danio rer
38		197.4	45.4	164631	14	BX901932	BX901932 Danio rer
c 39		197.4	45.4	165139	14	CR925756	CR925756 Danio rer
c 40		197.4	45.4	184799	14	CR936517	CR936517 Danio rer
c 41		197.4	45.4	186258	5	BX640480	BX640480 Zebrafish
42		197.4	45.4	224691	14	CR318603	CR318603 Danio rer
c 43		197.2	45.3	169758	5	CR936240	CR936240 Zebrafish
c 44		197.2	45.3	174623	5	BX005044	BX005044 Zebrafish
c 45		197	45.3	188775	14	CR855313	CR855313 Danio rer

ALIGNMENTS

RESULT 1
AF512998
LOCUS AF512998 2960 bp DNA linear VRT 10-JUL-2003
DEFINITION Danio rerio liver-type fatty acid binding protein gene, partial cds.
ACCESSION AF512998
VERSION AF512998.1 GI:21314558
KEYWORDS .
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 2960)
AUTHORS Her,G.M., Yeh,Y.H. and Wu,J.L.
TITLE 435-bp liver regulatory sequence in the liver fatty acid binding protein (L-FABP) gene is sufficient to modulate liver regional expression in transgenic zebrafish
JOURNAL Dev. Dyn. 227 (3), 347-356 (2003)
PUBMED 12815620
REFERENCE 2 (bases 1 to 2960)
AUTHORS Her,G.M. and Wu,J.-L.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2002) Institute of Zoology, Academia Sinica, 128, Yen-Chiu-Yuan Road, Sec. 2, Taipei 115, Taiwan
FEATURES Location/Qualifiers
source 1. .2960
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
mRNA <2784. .>2960
/product="liver-type fatty acid binding protein"
CDS 2784. .>2960
/note="Lfabp; small cytosolic protein involved in lipid transport and metabolism"
/codon_start=1
/product="liver-type fatty acid binding protein"
/protein_id="AAM47005.1"
/db_xref="GI:21314559"
/translation="MAFSGTWQVYAQENYEEFLRAISLPEEVIKLAKDVKPVTEIQQN GSDFTITSKTPGKTV"